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HUMAN
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                                          July 13, 2005, 08:01:55; Search time 90.0757 Seconds (without alignments) 2239.886 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                            rattus
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                         1612378 seqs, 512079187 residues
                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                       CIW3_HUMAN
CIW3_RAT
CIW3_MOUSE
Q9ESM5
                                                                                                                                                                                                                                                                                                                                                          CIW9 HUMAN
CIW9 CAVPO
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CIWF RAT
CIWF HUMAN
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CIWG HUMAN
Q8HYB8
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Maximum Match 100%
Listing first 45 summaries
                            OM protein - protein search, using sw model
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Q9ESM4
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1: uniprot_sprot:*
2: uniprot_trembl:*
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seq length: 200000000
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Match Length DB
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QBAVIS	CIWD HUMAN	Q6X6 <u>Z</u> 5	Q8BZB0	QBBUW1	CIWA HUMAN	CIWA_RAT	Q6Q834	Q6B014	Q6X6Z3	Q8I6M6	Q6PEI1	Q6X6Z4	Q801T4
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331	408	294	453	535	238	238	538	543	262	426	323	322	307
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	28	354	49.5	349.5	349.5	349.5	349.5	349.5	346.5	345.5	341	334.5	334
358.5	Э		ო	,									

ALIGNMENTS

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MEDLINE=2535313; PubMed=11680614;
A ABMMOL I., Goodwin P.A., Stanfield P.R.;
A REMINCLE 1., Goodwin P.A., Stanfield P.R.;
TASK-5, a novel member of the tandem pore K+ channel family.";
PILUGERS Arch. 442:828-833(2001)
-:- FUNCTION: pH-dependent, voltage-insensitive, background potassium channel protein. Rectification direction results from potassium concentration is protessium on either side of the membrane. Acts as an ion concentration on either side of the membrane. Acts as an outward rectifier when external potassium concentration is low. When external potassium concentration is high, current is inward.
C-:- SUBCELIULAR LOCATION: Integral membrane protein (Potential).
C-:- TISSUE SPECIFICITY: Widespread expression in adult. Strongest captersion in pancreas and placenta. Lower expression in brain, lung, prostate, heart, kidney, uterus, small intestine and colon.
-!- MISCELLANEOUS: Inhibited by external acidification. Activated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97459932; PubMed=9312005; DOI=10.1093/emboj/16.17.5464; Duprat F., Lesage F., Fink M., Reyes R., Heurteaux C., Lazdunski M.; "TASK, a human background K+ channel to sense external pH variations
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ACTIVATION.
MEDLINE=99254548; PubMed=10321245; DOI=10.1038/8084;
Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
"Inhalational anesthetics activate two-pore-domain background K+
                                                                                                                    16-OCT-2001 (Rel. 40, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Potassium channel subfamily K member 3 (Acid-sensitive potassium channel protein TASK-1) (TWIK-related acid-sensitive K+ channel 1)
(Two pore potassium channel KT3.1).
                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUBE-Heart,
Lopes C.M. Gallagher P.G., Buck M.E., Butler M.H.,
Goldstein S.A.N.;
"Proton block and voltage-gating are potassium-dependent in the
cardiac leak channel KCnk3.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
394 AA
                                                                                                                                                                                                                                                                                                                                          Name=KCNK3; Synonyme=TASK, TASK1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nat. Neurosci. 2:422-426(1999).
                                                                                16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           near physiological pH.";
EMBO J. 16:5464-5471(1997).
STANDARD;
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MUTAGENESIS OF HIS-98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELERVVLRLKPHKAGVQWRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYALLGIPL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 TLVMFQSLGERINTLVRYLLHRAKKGLGMRRADVSMANMVLIGFFSCISTLCIGAAAFSH 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 LVVLRFMTMNAEDEKRDAEHRALLTRNGQAGGGGGGGSAHTTDTASSTAAAGGGGFRNVY 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein; Ion transport; Ionic channel; Potassium;
Dobtssium channel; Transmembrane; Transport; Voltage-gated channel.
DOMAIN 1 8 Cytoplasmic (Potential).
TRANSMEM 9 29 Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytoplasmic (Potential).
N-linked (GlcNAc. .) (Potential).
H->N: Greatly reduces pH sensitivity.
halothane and isoflurane. SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.8) family.
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                                                                                                                                                                                                       GO; GO: 0005887; C: integral to plasma membrane; TAS. GO; GO: 0005267; F: potassium channel activity; TAS. GO; GO: 0006813; P: potassium ion transport; TAS. GO; GO: 0006813; P: potassium ion transport; TAS. GO; GO: 0007268; P: synaptic transmission; TAS. InterPro; IPR003280; K+channel_zpore. InterPro; IPR003280; K+channel_zpore. InterPro; IPR003092; TASK_channel. InterPro; IPR003092; TASK_channel. PR00309; IPR003092; TASK_channel. PR00309; ION trans; IPR003092; TASK_CHANNEL. PRINTS; PR01333; 2POREKCHANEL. PRINTS; PR01395; TASKCHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytoplasmic (Potential). Potential.
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                                                                                                                                                         EMBL; AF006823; AACS1777.1; -. EMBL; AF065163; AAG29340.1; -.
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Matches 394, Conservative
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MIM; 603220; -
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R RGD; 61997; Kcnk3.

R RGD; 61997; Kcnk3.

R RGD; 61997; Kcnk3.

R InterPro; IPR005221; Ion trans.

DR InterPro; IPR005406; TASK1 Channel Dore.

DR InterPro; IPR00520; TASK2 Channel.

DR Pfan; PF00520; Ion trans; 1.

DR Pfan; PF00520; Ion trans; 1.

DR PRINTS; PR0133; 2POREKCHANBE.

DR PRINTS; PR0139; TASKCHANNBE.

DR PRINTS; PR01095; TASKCHANNBE.

DR PRINTS; PR01095; TASKCHANNBE.

DR PRINTS; PR01095; TASKCHANNBE.

DR PRINTS; PR01095; TASKCHANNBE.

DR Qlycoprotein; Ion transport; Ionic channel; Potassium;

RW Glycoprotein; Ion transport; Ionic channel.

RW POCASSium channel; Transmembrane; Transport; Voltage-gated channel.

RW POCASSium channel; Pore-forming I (Potential).

101 Pore-forming I (Potential).
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Leonoudakis D., Gray A.T., Winegar B.D., Kindler C.H., Harada M.,
Leonoudakis D.M., Chavez R.A., Forsayeth J.R., Yost C.S.,
Taylor D.M., Chavez R.A., Forsayeth J.R., Yost C.S.,
"An open rectifier potassium channel with two pore domains in tandem cloned from rat cerebellum ";
J. Neurosci. 18:868-877(1998)
-! FUNCTION: PH-dependent, voltage-insensitive, background potassium channel protein. Rectification direction results from potassium ion concentration on either side of the membrane. Acts as an outward rectifier when external potassium concentration is low.
When external potassium concentration is high, current is inward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- MISCELLANEOUS: Inhibited by extracellular acidification, zinc, bupivacaine and phenytoin. Activated by protein kinase A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (By similarity).
SUBCELLULAR LOCATION: Integral membrane protein (Potential).
TISSUE SPECIFICITY: Strongest expression in heart. Moderate expression in lung and brain. Low levels in liver, kidney and skeletal muscle.
                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Potassium channel subfamily K member 3 (Acid sensitive potassium channel protein TASK-1) (THK-related acid-sensitive K+ channel 10 pore potassium channel TASK-1).
Name-Konk3; Synonyms=Task, Task1;
Rattus norvegicus (Rat).
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Potential.
Poter-forming 2 (Potential).
Cytoplasmic (Potential).
361 CLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394
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                                                                                                                                                                                                       STANDARD;
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ID CIW3_RAT
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last sequence update)
Potassium channel subfamily K member 3 (Acid-sensitive potassium channel protein TASK-1) (TWIK-related acid-sensitive K+ channel 1)
(Cardiac two-pore background K+ channel) (CTBAK-1) (Two pore potassium
                                                                                                                                                                           MKRQNVRTLALIVCTFTYLLVGAAVFDALESEPEMIERQRLELRQLELRARYNLSEGGYE
                                                                                                                                                                                                                                 BLERVVLRLKPHKAGVQWRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYALLGIPL
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                                                                                                     Gaps
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MEDLINE=9745992; PubMed=3912005; DOI=10.1093/emboj/16.17.5464;
MEDLINE=9745992: P. Pink M., Reyes R., Heurteaux C., Lazdunski M.;
"TASK, a human background K+ channel to sense external pH variations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S.A.;
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSPGGGGRYSDTPSRRCLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 HSSPGGGGRYSDTPSHPCLCSGTQRSAISSVSTGLHSLATFRGLMKRRSSV 411
N-linked (GlcNAc. . .) (Potential)
; D2778016E09E2BF5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lopes C.M., Gallagher P.G., Buck M.E., Butler M.H., Goldstein S. "Proton block and voltage gating are potassium-dependent in the cardiac leak channel Konk3.";
                                                                                                     17;
                                                                 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kim D., Fujita A., Horio Y., Kurachi Y.,
"Cloning and functional expression of a novel cardiac two-pore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20287574; PubMed=10748056; DOI=10.1074/jbc.M001948200;
                                                              DB 1; Length
                                                                                                     Indels
                                                                                                     23;
                                                                                  Pred. No. 2e-138;
8; Mismatches 2
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                                                          Query Match 90.6%; Score 1850.5; Best Local Similarity 88.3%; Pred. No. 2e-1 Matches 363; Conservative 8; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=Kcnk3; Synonyms=Ctbak, TASK, Task1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Biol. Chem. 275:16969-16978(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CTBAK-1).";
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MEDLINE=98165556; PubMed=9506712;
  53 N-
45276 MW;
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53
411 AA;
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CARBOHYD
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                        SUBURIT: Honodimer (Potential).
SUBURIT: Honodimer (Potential).
TISSUB SPECIFICITY: Very strong expression in heart, also detected in kidney, brain, skin, testis, lung, skeletal muscle, small intestine and stomach. Not detected in liver, thymus or spleen.
MISCELLANEOUS: Inactivated by barium.
SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.8) family.
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                                                                                                voltage-insensitive, background potassium
near physiological pH.";
EMBO 0. 16:5464-5471(1997).
-!- FUNCTION: pH-dependent, voltage-insensitive, background potassium
-!- channel protein. Rectification direction results from potassium
- ion concentration on either side of the membrane. Acts as an
- outward rectifier when external potassium concentration is low.

When external potassium concentration is high, current is inward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002801; Ion trans.
InterPro; IPR002801; K-Channel_2pore.
InterPro; IPR001280; K-channel_2pore.
InterPro; IPR001280; K-channel_pore.
InterPro; IPR0013092; TASK_channel.
Pfan, PR00250; Ion trans; I.
PRINTS; PR0133; 2POREKCHANEL.
PRINTS; PR0133; 2POREKCHANEL.
PRINTS; PR0195; TASKICHANNEL.
PR0195; 
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N-linked (GlcNAc. . .) (Potential).
Q -> E (In Ref. 3).
V -> I (in Ref. 3).
Ww, 35236E011AACS687 CRC64;
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Pred. No. 1.3e-137;
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EMBL; AF241798; AAF81418.1; -.
EMBL; AF242508; AAF81418.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF006824; AAC53367.1; -. EMBL; AB013345; BAA28349.1; -.
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88.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:1100509; Kcnk3.
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108
129
159
184
223
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WTFFQAYYYCFITLTTIGFGDYVALQXDQALQTQPQYVAFSFVYILTGLTVIGAFLNLVV 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RVVLRLKPHKAGVQWRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYALLGIPLTLV 121
                                                         282 GMGVGVGVGGGGFRNVYAEMLHFQSMCSCLMYKSREKLQYSIPMIIPRDLSTSDTCVEHS 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RVVLRLKPHKAGVQWRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYALLGIPLTLV 123
162 YERWTFPQAYYYCFITLTTIGFGDYVALQKDQALQTQPQYVAFSFVYILTGLTVIGAFLN 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----GGGGPRNVYAEVLHFQSMCSCLWYKSREKLQYSIPMIIPRDLSTSDTCVEQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 QNVRTLALIVCTFTYLLVGAAVFDALESEPELIERQRLELRQQELRARYNLSQGGYEELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aczmarek L.W.; Quinn A.M.; Wang L.-Y., Hughes T.,
A Gan L., Joiner W.J.; Quinn A.M.; Wang L.-Y., Hughes T.,
A Kaczmarek L.K.;
L. Submitted (SER-1997) to the EMBL/GenBank/DDBJ databasses.
-1- SIMILARITY: Belongs to the two pore domain potassium channel
C. (TC 1.A.1.8) family.
EMBL; AF022B21; AD09338.1; -.
R GD1, GO:0005615; C:extracellular space; TAS.
GO: GO:0005615; C:extracellular space; TAS.
R GO: GO:0005615; C:extracellular space; TAS.
InterPro; IPR001280; K-channel Dore.
InterPro; IPR001280; K-channel Dore.
InterPro; IPR001202; TASKI-channel.
InterPro; IPR001302; TASKI-channel.
R InterPro; IPR001302; TASKI-channel.
R PRINTS; PR01331; 2PGREKCHANEL.
R PRINTS; PR01331; 2PGREKCHANEL.
R PRINTS; PR01394; TASKICHANNEL.
R PRINTS; PR01955; TASKICHANNEL.
R PRINTS; PR01955; TASKICHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ion transport; Ionic channel; Transmembrane; Transport.

NON TER 1 1

NON TER 299 299

SEQUENCE 299 AA; 33325 MW; DCD41D8A212939C4 CRC64
                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UND-2003 (TrEMBLrel. 24, Last annotation update)
Putative potassium channel DP4 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65.3%; Score 1333; DB 2;
88.9%; Pred. No. 1.6e-97;
iive 7; Mismatches 18;
                                                                                                                                                                                                                                                                                           Ş
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Matches 263; Conservative
                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64
                                      241
                                                                      222
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Q9QX34;
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                                                                                                                                                           42 ELERVVIRLKPHKAGVOMRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYALLGIPL 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102 TLVMFQSLGERINTFVRYLLHRAKRGLGMRHAEVSMANMVLIGFVSCISTLCIGAAAFSY 161
                                                                                                       241 LIVILIREMTWINAEDEKRDAEHRALLTHNGQAVGLGGLSCLSGSLGDGVRPRDPVTCAAAAG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ELERVVLRLKPHKAGVQWRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYALLGIPL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 TLVMFQSLGERINTLVRYLLHRAKKGLGMRRADVSMANMVLIGFFSCISTLCIGAAAFSH 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKRONVRTLALIVCTFTYLLVGAAVFDALESEPELIERQRLELRQOELRARYNLSQGGYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LVVLRFMTMNAEDEKRDAEHRALLTRNGQAGGGG------GGSAHTTDTASSTAAA-
                                                                                                                                          ----GGGGFRNVYAEVLHFQSMCSCLWYKSREKLQYSIPMIIPRDLSTSDTCVEQSHS
                                                                                                                                                                                                                                                                                                                                                                                                                             Name-KNNK3b;
Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1155/2012 DEJULY (STEUKAWA M., Imaizumi Y.; Olya S., Kiteukawa M., Imaizumi Y.; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

1- SINILARITY: Belongs to the two pore domain potassium channel. CTC 1.A.1.8) family.

EMBL; AB048823; BAB16710.1; -.

EMBL; AB048823; BAB16710.1; -.

EMBL; AB048823; BAB16710.1; -.

R GO; GO:0005216; F:ion channel activity; IEA.

GO; GO:0005216; F:ion transport; IEA.

GO; GO:0006811; P:ion transport; IEA.

R GO; GO:000811; P:ion transport; IEA.

R D: GO:0006811; P:ion transport; IEA.

InterPro; IPR0013280; K+channel Zpore.

InterPro; IPR001380; K+channel Dore.

InterPro; IPR001380; TASKI channel.

InterPro; IPR001392; TASKI channel.

R PRINTS; PR01333; ZPOREKCHANNEL.

PRINTS; PR01934; TASKICHANNEL.

R PRINTS; PR01955; TASKICHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36;
                                                                                                                                                                                                                            361 SPGGGGRYSDTPSHPCLCSGTQRSAISSVSTGLHSLAAFRGLMKRRSSV 409
                                                                                                                                                                                                           346 SPGGGGRYSDTPSRRCLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84.8%; Score 1732; DB 2; Length 392;
83.9%; Pred. No. 4.8e-129;
ive 7; Mismatches 23; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ion transport; Ionic channel; Transmembrane; Transport
SEQUENCE 392 AA; 43150 MW; F5438B12AAD7FB1B CRC64;
                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
TASKL splice bvariant (TASKLb).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 83.9
Matches 345; Conservative
                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Brain;
                                                                         241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Richardson P.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 GLTVIGAFLNLVVLRFWTWNAEDEKRDAEHRALLTHNGQAGGLGGLSCLSGSLGDGVRPR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STSDTCVEQSHSSPGGGGRYSDTPSRRCLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSS 393
                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LCIGAAAFSHYEHWTFFQAYYYCFITLTTIGFGDYVALQXDQALQTQPQYVAFSFVYILT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLTVIGAFLNLVVLRFMTMNAEDEKRDAEHRALLTRNGQAGGGG------GGSAHTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MFYALLGI PLTLVMFOSLGERINTLVRYLLHRAKKGLGMRRADVSMANMVLIGFFSCIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DTASSTAAA-----GGGGFRNVYAEVLHFQSMCSCLWYKSREKLQYSIPMIIPRDL
 291
                     297
                                                                                                                                              Rattus norvėgicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
17;
                                                                                           01-MAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2003 (TrEMBLrel. 24, Last annotation update)
TWIK-related acid-sensitive K+ channel sprice variant (TASKIC)
                                                                                                                                                                                                                                                                                                                                                                                  2; Length 301;
                                                                                                                                                                                                SEQUENCE FROM N.A.
TIGASUEACTURA,
ONYAS., Kitsukawa M., Imaizumi Y.;
SEDURICTE (SEP-2000) to the EMBL/GenBank/DDBJ databases.
L. Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
R. GO, GO:0005216; Fintegral to membrane; IEA.
GO; GO:0005216; Fint channel activity; IEA.
R. GO; GO:0005216; Fiporassium channel activity; IEA.
R. GO; GO:0005216; Fiporassium in transport; IEA.
R. GO; GO:0005216; Fiporassium in transport; IEA.
R. GO; GO:0005216; Fiporassium channel activity; IEA.
R. GO: GO:0005216; Fiporassium in transport; IEA.
R. InterPro; IPR005406; TASKI channel.
R. InterPro; IPR005406; TASKI channel.
R. RINTS; PR015095; TASKICHANNEL.
R. PRINTS; PR01095; TASKCHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                        22; Indels
                                                                                                                                                                                                                                                                                                                                                              301 AA; 32811 MW; 265DE38DFA79595E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                  Score 1298.5; DB
Pred. No. 8.6e-95;
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                                                                                                                                                                                                                                                                                                                                                                                                       6; Mismatches
                                                                        301
                                                                                                                                                                                                                                                                                                                                                                                  63.6%;
85.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q63Z10,
Q63Z10;
25-OCT-2004 (TEMBLrel. 28,
25-OCT-2004 (TEMBLrel. 28,
25-OCT-2004 (TEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                  Query Match 63.6
Best Local Similarity 85.0
Matches 256; Conservative
                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         394 V 394
                                                                                                                                       Name=KCNK3c;
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 244
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                                                                                  09ESM4;
                                                   RESULT 6
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Q63ZIO
                                                              Q9ESM4
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Change 12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altachul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McZwan F.J., McKernan K.J., Mallek J.A., Gunarathe P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Makesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ELERVVLRLKPHKAGVQWRPAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYALLGIPL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLVMFQSLGERINTLVRYLLHRAKKGLGMRRADVSMANMVLIGFFSCISTLCIGAAAFSH 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LVVLRFWTWNAEDEKRDAEHRALLTRNGQAGGGGGGSAHTTDTASSTAAAGGGGFRNVY 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 LVVLRFLTMNSEDERRDAEERASL-----AGNRNSMIIHIQEDTPH------GRQRYK 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKRONVRTLSLIICTFTYLLVGAAVFDALBSDYEMREERKLKAEBIRLKGKYNISSEDYR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKRONVRTLALIVCTFTYLLVGAAVFDALESEPELIERORLELROQELRARYNLSQGGYE
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Xenopus laevis (African clawed 1rog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                  Clifton S.W.,
                                                                                                                                                                                                                                                                                                                                                        "Genetic and genomic tools for Xenopus research: The NIH Xenopus initiative.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20;
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                                                                                                                                                                                                                                                                MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
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Klein S., Gerhard D.S.;
Klein S., Gerhard D.S.;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC082937, AAH82937.1;
Hypothetical protein.
SROUENCE 374 AA; 42718 WW; 8F37D8FF1F689F63 CRC64;
                                                                                                                                                                                                                                                                                                  Klein S.L., Strausberg R.L., Wagner L., Pontius J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sci. U.S.A. 99:16899-16903(2002)
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; Pred. No. 6.6e-83;
47; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                             Dev. Dyn. 225:384-391(2002)
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Best Local Similarity 59.6%
Matches 235; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.
Proc. Natl. Acad. Sci. U.
                                                                                               Xenopodinae; Xenopus
NCBI_TaxID=8355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
288 AEVTDLQSVCSCMCYRSHE---YTSRMVSHQNSFSSKLNPQYFHSISYKIEEISPSTLKN 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          channel procein.
--- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
--- TISSUE SPECIFICITY: Mainly found in the cerebellum. Also found in adrenal gland, kidney and lung.
--- MISCELLANEOUS: Inhibited by phorbol 12-myristate 13-acetate (PMA).
Insensitive to changes in the pH range of 7-8.
--- SIMILARITY: Belongs to the two pore domain potassium channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Cerebellum;
PubMed=11043159; DOI=10.1016/S0169-328X(00)00183-2;
PubMed=11043159; DOI=10.1016/S0169-328X(00)00183-2;
Chapman C.G., Meadows H.J., Godden R.J., Campbell D.A., Duckworth M., Kelsell R.E., Murdock P.R., Randall A.D., Rennie G.I., Gloger I.S.;
"Cloning, localisation and functional expression of a novel human, erzebellum specific, two pore domain potassium channel.";
Brain Res. Mol. Brain Res. 82:74-83(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Girard C., Lesage F., Tinel N., Lazdunski M.;
"Human Task-3, a novel 2P domain potassium channel related to Task.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Neurophysiol. 86:130-142(2001).
-!- FUNCTION: pH-dependent, voltage-insensitive, background potassium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SECUENCE FROM N.A.
MEDLINE=20287530; PubMed=10747866; DOI=10.1074/jbc.M000030200;
Rajan S., Wischmeyer E., Liu G.X., Preisig-Mueller R., Daut J.,
Karschin A., Derst C.;
"TASK-3, a novel tandem pore domain acid-sensitive K+ channel. An
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Potassium channel subfamily K member 9 (Acid sensitive potassium channel subfamily K member 9 (Acid sensitive K+ channel 3 (Two pore potassium channel KT3.2)
Name=KCNK9; Synonyms=TASK3;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "KT3.2 and KT3.3, two novel human two-pore K(+) channels closely related to TASK-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-21324619; PubMed-11431495;
Vega-Saenz de Miera E., Lau D.H.P., Zhadina M., Pountney D.,
                                                     361 CLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394
                                                                                       | :|||| |||| :
|----SPVSSVSPGLHSFTDKHRLMKRRKSI 374
                                                                                                                                                                                                                                              374 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         extracellular histidine as pH sensor.";
J. Biol. Chem. 275:16650-16657(2000).
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                                                                                                                                                                                                                                              STANDARD;
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TLVMFQSLGERINTLVRYLLHRAKKGLGMRRADVSMANMVLIGFFSCISTLCIGAAAFSH 180
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 44, Last annotation update)
Potassium channel subfamily K member 9 (Acid-sensitive potassium channel protein TASK:3) (TWIK-related acid-sensitive K+ channel 3).
Name=KCNK9; Synonyms=TASK3;
Cavia porcellus (Guinea pig).
                                                                                                                                                                                                                                                                                        Glycoprotein; Ion transport; Ionic channel; Potassium; obcissium channel; Transmembrane; Transport; Voltage-gated channel. DOMAIN 1 8 Cytoplasmic (Potential) 9 29 Potential.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.7%; Score 1116; DB 1; Length 374; 59.0%; Pred. No. 3.3e-80; ive 44; Mismatches 96; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pore-forming 2 (Potential).
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Potential.
Cytoplasmic (Potential).
Potential.
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MW, 8A19EAEE5A4D7F38 CRC64;
            MIM; 608074; -.

GO; GO:0005624; C:membrane fraction; NAS.
GO; GO:0005627; F:potassium channel activity; NAS.
GO; GO:0005813; P:potassium ion transport; NAS.
GO; GO:0006813; P:potassium ion transport; NAS.
INTEPPO; IRR005821; Ion trans.
INTEPPO; IRR00380; K+channel_pore.
INTEPPO; IRR003092; TASK_channel.
INTEPPO; IRR003092; TASK_channel.
Pfam; PF00520; Ion trans; 1.
PRINTS; PR0133; 2FOREKCHANEL.
PRINTS; PR01985; TASKCHANNEL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       360 RCLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394
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Genew; HGNC:6283; KCNK9
MIM; 605874; -
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101
128
158
179
207
239
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240
53
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RY MEDILINE=21864514; PubMed=11875121; DOI=10.1210/me.16.3.621;
RX MEDILINE=21864514; PubMed=11875121; DOI=10.1210/me.16.3.621;
RX GITJAR C. Enyedin P.;
RY TASK-3 Dominates the Background Potassium Conductance in Rat Adrenal
RT Glomerulosa Cells.";
RI Mol. Endocrinol. 16:621-629(2002).
CC --- SIMILARITY: Belongs to the two pore domain potassium channel
CC (TC 1.A.1.8) family.
DR GO; GO:0016021; C:inteqsal to membrane; IEA.
DR GO; GO:0016021; C:inteqsal to membrane; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR RO; GO:0006813; P:potassium ion transport; IEA.
DR PRINTS; PR01383; ZPOREKCHANEL.
DR PRINTS; PR01985; TASKSCHANNEL.
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                      299 VYAEVLHFQSMCSCLWYKSREKLQYSIPMIIPRDLSTSDTCVEQSHSSPGGGGRYSDTPS 358
                                                              -----SPS 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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                                             -----DLQSVCSCACYRSQP--QNFGATLAPQPLHSISCRIEEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ion transport; Ionic channel; Transmembrane; Transport. SEQUENCE 396 AA; 44357 MW; 734EBOEEA1ED1828 CRC64;
                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                   365
                                                                                                            RRCLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394
                                                                                                                                                   332 --TLKNSLFPSPISSVSPGLHSFGDNHRLMLRRKSV
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01-DEC-2001 (TrEMBLrel. 19,
01-JUN-2003 (TrEMBLrel. 24,
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Best Local Similarity 70.8<sup>3</sup>
Matches 189; Conservative
                                                                                                                                                                                                                                                                                                                                                                           Potassium channel TASK-3.
                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                  Name=Kcnk9;
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                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb.ch).
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                                                                                                                       MEDLINE=2028/530; PubMed=10747866; DOI=10.1074/jbc.M000030200; Rajan S., Wischmeyer E., Liu G.X., Preisig-Mueller R., Daut J., Karschin A., Derst C.;
"TASK-3, a novel randem pore domain acid-sensitive K+ channel. An extracellular histidine as pH sensor.";
J. Blol. Chem. 275:16650-16657(2000).
-!- FUNCTION: pH-dependent, voltage-insensitive, background potassium channel protein.
-!- SIMILABLIY: Belongs to the two pore domain potassium channel
(TC 1.A.1.8) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKRQNVRTLALIVCTFTYLLVGAAVFDALESEPELIERQRLELRQQELRARYNLSQGGYE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein; Ion transport; Ionic channel; Potassium;
Potassium channel; Transmembrane; Transport; Voltage-gated channel.
DOMAIN
1 8 Cytoplasmic (Potential).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Hystricognathi, Caviidae, Cavia.
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N-linked (GlcNAc. . .) (Potential).
261DC973FF53AF91 CRC64;
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Potential.
Pore-forming 2 (Potential).
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Pore-forming 1 (Potential)
Potential.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR005821; Ion trans.
InterPro; IPR00380; K+channel_Zpore.
InterPro; IPR001622; K+channel_Dore.
InterPro; IPR005407; TASK3 channel.
InterPro; IPR003092; TASK channel.
Pfam; PF00520; Ion trans; I.
PRINTS; PR0133; ZPOREKCHANEL.
PRINTS; PR01585; TASK3CHANNEL.
PRINTS; PR01095; TASKGCHANNEL.
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40769 MW;
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Best Local Similarity 57.1%
Matches 226; Conservative
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219
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365 AA;
                                                                                     FROM N.A.
                                       NCBI_TaxID=10141;
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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STRAIN=Sprague-Dawley; TISSUE=Cerebellum;
Kim Y.M., Bang H.W., Kim D.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
-! - SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.8) family.
                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Sprague-Dawley; TISSUE=Cerebellum;
MEDLINE=20200422; PubMed=10734076; DOI=10.1074/jbc.275.13.9340;
Kim Y., Bang H., Kim D.;
Kim X., Bang H., Kim D.;
"TASK-3, a New Member of the Tandem Pore K+ Channel Family.";
J. Biol. Chem. 275:9340-9347(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 395;
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InterPro; IRRO03200; K-channel 2pore.
InterPro; IRRO03200; K-channel 2pore.
InterPro; IRRO03092; K-channel 2pore.
InterPro; IRRO03092; TASK Channel.
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                                                                                                          Last sequence update)
Last annotation update)
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GO:0016021; C:integral to membrane; IEA.
GO:0005216; F:ion channel activity; IEA.
GO:0005267; F:potassium channel activity; IEA.
GO:0006811; F:ion transport; IEA.
GO:0006813; P:potassium ion transport; IEA.
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69.7%; Pred. No. 7.6e-68;
iive 31; Mismatches 49
       395 AA
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(Rel. 41, Last sequence update)
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                                                                            Created)
   PRT;
                                                                    01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 69.79
Matches 186; Conservative
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   PRELIMINARY;
                                                                                                                                                                                   Potassium channel TASK3.
                                                                                                                                                                                                                            Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
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Q9ES08;
28-FEB-2003 (
28-FEB-2003 (
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ID CIW9
AC Q9ES
DT 28-F
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                                              channel protein TASK-3) (Two pore potassium channel KT3.2) (Fragment). Name=KCnk9; Synonyms=Task3; Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       auditory nervous system.";
Mol. Cell. Neurosci. 18:632-648(2001).
-!- FUNCTION: pH-dependent, voltage-insensitive, background potassium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           channel protein.

-!-SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!-TISSUE SPECIPICITY: Expressed in the CNS but not in heart, lung, liver, kidney, intestine and skeletal muscle. The highest expression was found in the olfactory nuclei, piriform cortex, cerebellum, antedorsal thalmic nucleus, pontine nucleus, dorsal raphe and several nuclei in the medulla. Shows a non-homogeneous distribution in the hippocampus. Expressed at highest levels in the lateral posterior and inferior portions and at medium levels
                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21624462; PubMed=11749039; DOI=10.1006/mcne.2001.1045; Karschin C., Wischmeyer E., Preisig-Mueller R., Rajan S., Derst C., Grzeschik K.-H., Daut J., Karschin A.; Expression pattern in brain of TASK-1, TASK-3, and a tandem pore domain K(+) channel subunit, TASK-5, associated with the central
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Potassium channel; Transmembrane; Transport; Voltage-gated channel.
DOMAIN 1 8 Cytoplasmic (Potential).
05-JUL-2004 (Rel. 44, Last annotation update)
Potassium channel subfamily K member 9 (Acid-sensitive potassium
                                                                                                                                                                                                                                                                                                                                                                                                  Vega-Saenz de Miera E., Lau D.H.P., Zhadina M., Pountney D., Coetzee W.A., Rudy B.;
"Kt3.2 and kt3.3, two novel human two-pore k(+) channels closely related to TASK-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.8) family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pore-forming 2 (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytoplasmic (Potential).
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Pred. No. 3.3e-65;
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Interpro; IPR001622; K+channel_pore.
Interpro; IPR001622; K+channel_pore.
Interpro; IPR003092; TASK_channel.
INTERPRO; PR0133; ZPOREKCHANEL.
PRINTS; PR01585; TASKCHANNEL.
PRINTS; PR01095; TASKCHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Potentia]
                                                                                                                                                                                                                                                                                                                                            STRAIN=Sprague-Dawley;
MEDLINE=21324619; PubMed=11431495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Neurophysiol. 86:130-142(2001).
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101
128
158
179
207
207
537
237
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                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                       ELERVVLRLKPHKAGVQWRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYALLGIPL 120
                                                                                                                         TLVMFQSLGERINTLVRYLLHRAKKGLGMRRADVSMANMVLIGFFSCISTLCIGAAAFSH 180
                                                                                                                                                                                              TLVMFQSLGERMNTFVRYLLKRIKKCCGMRNTEVSMENMVTVGFFSCMGTLCLGAAAFSQ 180
                                  9
                                                    YEHWTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQYVAFSFVYILTGLTVIGA 237
                                                                                                                                                                                                                                                                               237
                                  1 MKRONVRTLALIVCTFTYLLVGAAVFDALESEPELIERQRLELRQQELRARYNLSQGGYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      auditory nervous system.";

Mol. Cell. Neurosci. 18:632-648(2001).

-!- FUNCTION: Probable potassium channel subunit. No channel activity observed in heterologous systems. May need to associate with another protein to form a functional channel.
-!- SUBUNIT: Heterodimer (Potential).
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: Brain-specific. Highly expressed in auditory nuclei, in Purkinje cells and in olfactory bulb mitral cells.
-!- SIMILARITY: Belongs to the two pore domain potassium channel
(TC 1.A.1.8) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21624462; PubMed=11749039; DOI=10.1006/mcne.2001.1045; Karschin C., Wischmeyer E., Preisis-Mueller R., Rajan S., Derst C., Grzeschik K.-H., Daut J., Karschin A., Expression pattern in brain of TASK-1, TASK-3, and a tandem pore domain K(+) channel subunit, TASK-5, associated with the central
                                                                                                                                                                                                                                                             181 CEDWSFFHAYYYCFITLTTIGFGDFVALQSKGALQRKPFYVAFSFMYILVGLTVIGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         potassium
channel 5)
 °,
37; Indels
                                                                                                                                                                                                                                                                                                                                                                               QBR510; Q920G1;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-ULL-2004 (Rel. 44, Last annotation update)
Potassium channel subfamily K member 15 (Acid-sensitive phannel protein TASK-5) (TWIK-related acid-sensitive K+ (Channel Protein TASK-5) (TWIK-related acid-sensitive TASK-5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRALIB-LONG Evanns, TISSUE-Brain,
Kawano T., Nakajima S., Nakajima Y.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                  318 AA
26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR005821; Ion trans.
InterPro; IPR003280; K+channel_2pore.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF467250; AAL77036.1; -.
EMBL; AF294353; AAK97094.1; -.
RGD; 619733; Kcnk15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=Kcnk15; Synonyms=Task5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 82-318 FROM N.A.
Conservative
                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
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Matches
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LTLVMFQSLGERINTLVRYLLHRAKKGLGMRRADVSMANMVLIGFFSCISTLCIGAAAFS 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53
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TISSUE=Brain, Colon, and Ovarian carcinoma; MEDLINE=21624462; PubMed=11749039; DOI=10.1006/mcne.2001.1045;

Karschin C., Wischmeyer E., Preisig-Mueller R., Rajan S., Derst C., Grzeschik K.-H., Daut J., Karschin A., Rayan S., Derst C., "Expression pattern in brain of TASK-1, TASK-3, and a tandem pore domain K(+) channel subunit, TASK-5, associated with the central
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 EELERVVLRLKPHKAGVQWRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYALLGIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 HYBHWIFFQAYYYCFIILITIGFGDYVALQKDQALQTQPQYVAFSFVYILIGLTVIGAFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKRQNVRTLALIVCTFTYLLVGAAVFDALESEPELIERQRLELRQQ-ELRARYNLSQGGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USH427; QSHBC8; Created)
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2004 (Rel. 44, Last annotation update)
Potassium channel subfamily K member 15 (Acid-sensitive potassium channel protein TASK-5) (TWIK-related acid-sensitive K+ channel 5)
(Two pore potassium channel KT3.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.9%; Score 916.5; DB 1; Length 318; 68.8%; Pred. No. 1.8e-64; ive 29; Mismatches 52; Indels 3.
                                                                                                                                                                      Ion transport; Ionic channel; Potassium; Potassium channel;
Transmembrane; Transport; Voltage-gated channel.
DOMAIN
1
Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                   Pore-forming 2 (Potential)
                                                                                                                                                                                                                                                                 Pore-forming 1 (Potential) Potential.
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A0629212F56834ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                   Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                   Cytoplasmic (Potential). Potential.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          al Similarity 68.8%; Pred. No. 1.8e 185; Conservative 29; Mismatches
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                                                                                                                                                                                                                                                  Potential.
                                                                                                                                                                                                                                                                                                                                                                                             Potential.
InterPro; IPR001622; K+channel pore.
InterPro; IPR008073; TASK5_channel.
InterPro; IPR003092; TASK_channel.
Pfam; PF00520; Ion_trans; I.
PRINTS; PR01333; 2POREKCHANEL.
PRINTS; PR01690; TASK5CHANNEL.
PRINTS; PR01095; TASKCHANNEL.
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Mol. Cell. Neurosci. 18:632-648(2001)
                                                                                                                                                                                                                                                                                                                                                                                        243 Pol
318 Cyr
315 R
35651 MW;
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                                                                                                                                                                                                                                                                      80
108
129
189
223
243
315
318 AA;
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Matches 167; Conservative
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REQUENCE FROM N.A., AND VARIANTS GLU-95; THR-260 AND LEU-323.

REDINE=21638749; PubMed=11780052; DOI=10.1038/414865a;

REDINE=21638749; PubMed=11780052; DOI=10.1038/414865a;

REDINE=21638749; PubMed=11780052; DOI=10.1038/414865a;

REDINES=21638749; PubMed=11780052; DOI=10.1038/414865a;

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REDING DOI-10.10.10.

REDING DOI-10.10.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Coetzee W.A., Rudy B.;
"KT3.2 and KT3.3, two novel human two-pore K(+) channels closely related to TASK-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and spleen.
SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.8) family.
                                                                                                                                                                                                Ashmole I., Goodwin P.A., Stanfield P.R.;
"TASK-5, a novel member of the tandem pore K+ channel family.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                       Jega-Saenz de Miera E., Lau D.H.P., Zhadina M., Pountney D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003280; K+channel_2pore.
InterPro; IPR001622; K+channel_pore.
InterPro; IPR008073; TASK5_channel.
                                       MEDLINE=21324619; PubMed=11431495;
                                                                                                                                      J. Neurophysiol. 86:130-142(2001)
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SEQUENCE FROM N.A.
                                                                                                                                                                           SEQUENCE FROM N.A.
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                    rissum=Brain;
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EMBL; EMBL; EMBL; EMBL;

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YEHWIFFQAYYYCFIILITIGFGDYVALQKDQALQTQPQYVAFSFVYILIGLTVIGAFLN 240
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01-07T-2004 (TrEMBLrel. 18, Last sequence update)
25-00T-2004 (TrEMBLrel. 28, Last annotation update)
Suppressor protein 9 (Putative potassium channel subunit n2P38) (Twopore K+ channel).
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                     ane, Transport, Voltage-gated channel. Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           functional expression.
W->R: No effect on lack of functional
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                                                                                                                                                                                                                                                                                  Pore-forming 2 (Potential)
                                                                                                                                                                                          Pore-forming 1 (Potential)
InterPro; IPR003092; TASK channel.
PRINTS; PR01333; 2POREKCHÄNEL.
PRINTS; PR01690; TASKSCHANNEL.
PRINTS; PR01595; TASKTCHANNEL.
Ion transport; Ionic channel; Polymorphism; Potassium;
Potassium channel; Transmembrane; Transport; Voltage-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         330 AA; 36130 MW; AA2A54D0615BC53C CRC64;
                                                                                                                                                                                                                                                                                                                           Cytoplasmic (Potential).
                                                                                                                                                                                                                                     Cytoplasmic (Potential). Potential.
                                                                                                                                                                                                                                                                                                                                                   G -> E (in TASK-5B).

/FIG=VAR 014211.
P -> T (in TASK-5B).
/FTIG=VAR 014212.
P -> H (in TASK-5A).
/FTIG=VAR 014213.
P -> L (in TASK-5A).
/FTIG=VAR 014213.
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LVVLRFLVASADWPERAA 258
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Caenorhabditis elegans.
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Query Match 40.2%; Score 820; DB 2; Length 329;
Best Local Similarity 48.3%; Pred. No. 8.5e-57;
Matches 172; Conservative 54; Mismatches 84; Indels 46; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Perez de la Carz I., Horvitz H.R.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the two pore domain potassium channel
(TC 1.A.1.8) family.
EMBL; AF025454; AAC71151.2; --
EMBL; AF0357729; AAC71151.2; --
EMBL; AX357729; AAC32863.1; -.
PIR; T32347; T32347.
WormBase; WBGene00006318; sup-9.
                                                                      Wormbase Consortium;
"Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
Science 282:2012-2018(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO, GO: 0016020; C: membrane; IEA.
GO, GO: 0016020; C: membrane; IEA.
GO; GO: 0016216; F: ion channel activity; IEA.
GO; GO: 0006217; F: potassium channel activity; IEA.
GO; GO: 0006811; F: ion transport; IEA.
GO; GO: 0006811; P: potassium ion transport; IEA.
InterPro; IPR0018280; K+channel_zore.
InterPro; IPR001622; K+channel_zore.
InterPro; IPR001622; K+channel_zore.
InterPro; IPR001829; TASK_channel.
FEan; PR0133; 2POREKCHANEL.
PRINTS; PR0133; 2POREKCHANEL.
PRINTS; PR01095; TASKCHANNEL.
PRINTS; PR01095; TASKCHANNEL.
PRINTS; PR01095; TASKCHANNEL.
PRINTS; PR01095; TASKCHANNEL.
SEQUENCE 329 AA; 36992 MW; 338A6D9A577464CD CRC64;
                                                                                                                                                                                                                                                                         STRAIN=Bristol N2;
Murray J., Wohldmann P., O'Neal D.;
"The sequence of C. elegans cosmid F34D5.";
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Waterston R.; Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Wormbase Consortium;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Wang Z.-W., Salkoff L.;
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
STRAIN-Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Neurosci. 23:9133-9145(2003).
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Submitted (JUN-2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=Bristol N2;
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SHYEHWTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQYVAFSFVYILTGLTVIGAF 238
                                                                                                                                                                                                        61 ELERVVLRLKPHKAGVQWRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYALLGIPL 120
                                                                                         121 TLVMFQSLGERINTLVRYLLHRAKKGLGMRRADVSMANMVLJGFFSCISTLCI--GAAAF 178
                                                                                                                                                                                          239 LNLVVLRFMTMNAEDEKRDAEHRAL----LTRNGQAGGGGGGGSAHTTDTASSTAAAGGG 294
295 GPRNVYAEVLHFQSMCSCLWYKSREKLQYSIPMIIPRDLSTSDTCVEQSHSSPGGG 350
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Search completed: July 13, 2005, 08:44:33 Job time: 92.0757 secs

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Aam14676 Abb33636

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Peptide

Human pep Amino aci Drosophil Human NOV

Aam27095
Abb280454
Abb280454
Abb1908045
Aam54409
Abg48478
Abg389
Abg3804
Abb717787
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Murine TR A mechani A mechani Mouse h-T

Amino aci Mouse can

us-09-503-089a-5.rag

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The invention relates to human and mouse TREK-1 potassium channel proteins and their corresponding DNA molecules. TREK-1 nucleic acid is useful for transfecting cells to induce expression of the TREK-1 potassium channel protein. These cells are then used in assays to identify compounds which have anaesthetic properties, producing a safe, reversible state of unconsciousness with concurrent amnesia and analgesia in a mammal upon inhalation. The present sequence is murine TASK potassium channel protein related to the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murine; potassium channel protein; TREK-1; TASK; anaesthetic; analgesia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel nucleic acid encoding a TREK-1 potassium channel protein for transfecting cells to be used to identify compounds with anesthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 2042;
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                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murine TASK potassium channel protein.
                                                        AAM27095
ABB28454
ABB28454
AAB28456
AAM6810
AAM62399
ABG3465
ABG3465
ABB71787
ABD14995
ABO14995
ABO1495
                             AAM14676
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                                                                                                                                                                                                                                                                                                                                                                                                   AAE10343 standard; protein; 394 AA
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11-FEB-2000; 2000US-00503089.
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Honore E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-549146/50.
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                           AAE10343;
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 Human pot
Human sig
Human pro
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New nucleic acid encoding a non-inactivating outwardly rectifying potassium transport channel, designated TASK2, useful in the treatment of hypertension or dysfunctions of the kidney, liver or pancreas.
                                                                                                                                                                                                    The present sequence is that of human TASKI (TWIK-related acid-sensitive K+ channel), a member of a new family of 2P domain potassium channels, also including TWIK-1 (see AAY79673) and novel TASK2 (see AAY79675).

TASKI is expressed in many different tissues, and at particularly high levels in pancreas and placenta. Host cells expressing TWIK-1 family members can be used to screen for substances that modulate the activity of members of the TWIK-1 family of potassium channels. The drugs identified may be useful in the treatment of diseases of the heart or of the nervous system, such as epilepsy, arrhythmia, vascular diseases, neurodegenerative diseases, kidney, liver or pancreas diseases, hypertension, diseases associated with ischaemia or anoxia, endocrine diseases associated with ischaemia or anoxia, endocrine diseases.
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inflammation; cardiovascular disease; anticioancer; anti-inflammatory;
antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic;
antiasthmatic; gene therapy; cell proliferation; neurological disorder;
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100.0%; Pred. No. 5.3e-213;
ive 0; Mismatches 0;
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                                                                                                                                                 Disclosure, Fig 8, 91pp, English
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301 AEVLHPQSMCSCLMYKSREKLQYSIPMIIPRDLSTSDTCVEQSHSSPGGGGRYSDTPSRR 360
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      121 TLVMFQSLGERINTLVRYLLHRAKKGLGMRRADVSMANMVLIGFFSCISTLCIGAAAFSH
                            121 TLVMFQSLGERINTLVRYLLHRAKKGLGMRRADVSMANMVLIGFFSCISTLCIGAAAFSH
                                                                                                                            YEHWTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQYVAFSFVYILTGLTVIGAFLN
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                                                                                       YEHWTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQYVAFSFVYILTGLTVIGAFLN
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                                                                                                                                                                                                                                                                                                                                          CLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394
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2000US-0235018P.
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15-DEC-2000; 2
18-DEC-2000; 2
21-DEC-2000; 2
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07-APR-2000;
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25-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human signal peptide-containing proteins useful in treatment, prevention and diagnosis of e.g. cancer, inflammation and cardiovascular
reproductive disorder, developmental disorder; arteriosclerosis; cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia; asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia; Parkinson's disease; Huntington's diseases; ovulatory defect;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baughn MR;
i, Hillman JL;
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H, Patterson C, Reddy R,
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100.0%; Pred. No. 5.3e-213;
ive 0; Mismatches 0;
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98US-0094983P.
98US-0102686P.
98US-0112129P.
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Matches 394; Conservative
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                                                                                       muscular dystrophy
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                                                                                                                                                                        WO200000610-A2
                                                                                                                                 Homo sapiens.
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01-OCT-1998
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The invention relates to TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611,

IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and 53763 ion channel
family (ICF) mucleic acids and proteins. The FWIK-6, TWIK-7, IC23927,

TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and
53763 ICF nucleic acids and proteins may be used for preventing,
catagnosing and treating ICF-related diseases. The sequences may be used
to treat disorders associated with decreased expression by rectifying
cutations or deletions in a patient's genome that affect the activity of
the proteins by expressing inactive proteins or to supplement the
complement own production of ICF proteins. The proteins and in
the production of ICF proteins. The proteins and in
catigens in the production of antibodies against ICF proteins and in
catigens in the production of antibodies against ICF proteins and in
catigens in the production of ICF proteins. The proteins may be used to
anti-ICF protein antibodies, agonists and antagonists may be used to
regulate ICF protein expression and activity. The antibodies may also be
consed as diagnose and treat a wide variety of disorders, e.g. cancers
cond leukaemia, Alzheimer's disease, Parkinson's disease, multiple
cond leukaemia, Alzheimer's disease, Parkinson's disease, multiple
cond leukaemia Alpha for this patent is also available in electronic
cond leukaemia Alpha Alpha
e.g. cancers, Alzheimer's disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  format from USPTO at segdata.uspto.gov/sequence.html
                                                                                                                Disclosure; SEQ ID NO 17; 638pp; English
    treating
preventing, diagnosing and cardiovascular disorders.
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                                                                            1 MKRQNVRTLALIVCTFTYLLVGAAVFDALESEPELIERQRLELRQQELRARYNLSQGYE
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                                        Gaps
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0
  Length 394;
                                      Indels
100.0%; Score 2042; DB 8;
llarity 100.0%; Pred. No. 5.3e-213;
Conservative 0; Mismatches 0;
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                    Best Local Similarity
Matches 394; Conserv
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  Query Match
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                                                     ADI27925 standard; protein; 394
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Length 394;

DB 8;

Score 2042;

100.08;

Sequence 394 AA;

Query Match

format from USPTO at segdata.uspto.gov/sequence.html

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The invention relates to TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and 53763 ion channel IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, FWIK-7, IC23927, TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and 53763 ICF nucleic acids and proteins may be used for preventing. Contract disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of ICF proteins by expressing inactive proteins or to supplement the patients own production of ICF proteins. The proteins may also be used as anti-ICF protein antibodies, against ICF proteins and in anti-ICF protein antibodies, againsts may be used to regulate ICF protein expression and activity. The anti-ICF protein expression and activity. The regulate ICF protein expression and activity. The regulate ICF protein expression and activity. The antibodies may also be used to regulate ICF protein expression and activity. The antibodies may also be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9, alpha2delta-4, 54414, or 53763 nucleic acids and proteins, useful for preventing, diagnosing and treating e.g. cancers, Alzheimer's disease and cardiovascular disorders.
Human; ion channel family; ICF; cancer; leukaemia; Alzheimer's disease; Parkinson's disease; multiple sclerosis; epilepsy; hepatic disorder; cardiovascular disorder; cytostatic; neuroprotective; nootropic; antiparkinsonian; hepatotropic; cardiovascular.
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2000US-0233537P.
2000US-0235018P.
2000US-0235059P.
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07-APR-2000;
11-APR-2000;
26-APR-2000;
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                              1 MKRONVRTLALIVCTFTYLLVGAAVFDALESEPELIERQRLELRQQELRARYNLSQGGYE
                                         BLERVVLRLKPHKAGVQWRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYALLGIPL
                                                                        TLVMFQSLGERINTLVRYLLHRAKKGLGMRRADVSMANMVLIGFFSCISTLCIGAAAFSH
                                                                                                        YEHWTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQYVAFSFVYILTGLTVIGAFLN
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2000US-0518866.
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               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            anti-ICF protein antibodies, agonists and antagonists may be used to regulate ICF protein expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of ICF proteins in samples (e.g. by immunoassay). The nucleic acids and proteins may be used to prevent, diagnose and treat a wide variety of disorders, e.g. cancers and leukaemia, Alzheimer's disease, Parkinson's disease, multiple sequence represents a human protein used in the scope of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at seqdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                       TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9, applaadelta-4, 5414, or 53763 nucleic acids and proteins, useful for preventing, diagnosing and treating e.g. cancers, Alzheimer's disease and cardiovascular disorders.
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100.0%; Pred. No. 5.3e-213;
ive 0; Mismatches 0;
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25-SEP-2001; 2001US-00964256 17-DEC-2001; 2001US-00024623
                                                                                                                     (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                Curtis RAJ, Glucksmann MA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615, HNWDA-1, TWIK-9, alphaldelta-4, 54414, or 53763 nucleic acids and proteins, useful for preventing, diagnosing and treating e.g. cancers, Alzheimer's disease cardiovascular disorders.
                                                                                                                        Rat; ion channel family; ICF; cancer; leukaemia; Alzheimer's disease; Parkinson's disease; multiple sclerosis; epilepsy; hepatic disorder; cardiovascular disorder; cytostatic; neuroprotective; nootropic; antiparkinsonian; hepatotropic; cardiovascular.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glucksmann MA, Silos-Santiago I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 9; 638pp; English
                                  ADI27916 standard; protein; 412 AA
                                                                                                                                                                                                                                                                                                                       200005-0195993P.
200005-0195933P.
200005-023537P.
200005-0235059P.
200005-0256240P.
200005-025658P.
200005-025658P.
200105-0059635.
200105-00828035.
                                                                                                                                                                                                                                                                                        2000US-0185938P.
2000US-00518866.
2000US-0195734P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001US-00957683.
2001US-00964252.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       001US-00964256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-DEC-2001; 2001US-00024623
                                                                                                                                                                                                                                                      15-MAY-2002; 2002US-00146733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MILL-) MILLENNIUM PHARM INC
                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-069000/07
                                                                                                                                                                                    Rattus norvegicus
                                                                                                                                                                                                           US2003165891-A1.
                                                                                                      protein #1
                                                                                                                                                                                                                                                                                                                                                            25-SEP-2000;
25-SEP-2000;
15-DEC-2000;
18-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                         21-DEC-2000;
28-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                06-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-SEP-2001;
                                                                                                                                                                                                                                                                                                                           11-APR-2000;
26-APR-2000;
                                                                                                                                                                                                                                                                                                                                                 19-SEP-2000;
                                                                                                                                                                                                                                                                                                     03-MAR-2000;
                                                                                                                                                                                                                                                                                                                 07-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-SEP-2001;
                                                                                06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Curtis RAJ,
                                                                                                                                                                                                                                  04-SEP-2003
                                                         ADI27916;
                        ADI27916
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samples (e.g. by immunoassay). The nucleic acids and proteins may be used to prevent, diagnose and treat a wide variety of disorders, e.g. cancers and leukaemia, Alzheimer's disease, Parkinson's disease, multiple sclerosis, epilepsy, hepatic disorders and cardiovascular disorders. This sequence represents a rat protein used in the scope of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at seqdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLVMFQSLGERINTLVRYLLHRAKKGLGMRRADVSMANMVLIGFFSCISTLCIGAAAFSH 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     242 LVVIRFMTWNAEDEKRDAEHRALLTHNGQAGGLGGLSCLSGSLGDGVRPRDPVTCAAAG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361
                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TASK; TWIK-related acid-sensitive K+ channel; mouse; potassium channel;
                                                                                                                                                                                                                                                                                                                                                                                                                          2 MKRQNVRTLALIVCTFTYLLVGAAVFDALESEPEMIERQRLEERQLEERARYNLSBGGYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELERVVIRLKPHKAGVQWRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYALLGIPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 YERWITEPQAYYYCPITLITIGFGDYVALQKDQALQTQPQYVAFSFVYILTGLTVIGAFLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GMGVGVGVGGGGGFRNVYAEMLHFQSMCSCLMYKSREKLQYSIPMIIPRDLSTSDTCVEHS
                                                                                                                                                                                                                                                                                                                                                                                          1 MKRQNVRTLALIVCTFTYLLVGAAVFDALESEPELIERQRLELRQQELRARYNLSQGGYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELERVVLRLKPHKAGVQWRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYALLGIPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YEHWTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQYVAFSFVYILTGLTVIGAFLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LVVLRFMTMNAEDEKRDAEHRALLTRNGOAGGGGG-----GGSAHTTDTASSTAAA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----GGGGFRNVYAEVLHFQSMCSCLWYKSREKLQYSIPMIIPRDLSTSDTCVEQS
                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            drug screening; hypertension; hypotensive; epilepsy; arrhythmia; vascular diseases; neurodegenerative disease; ischaemia; anoxia; endocrine disease; muscle disease; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSPGGGGRYSDTPSRRCLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394
                                                                                                                                                                                                                                                                                                                                     17;
                                                                                                                                                                                                                                                                                DB 8; Length 412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23; Indels
                                                                                                                                                                                                                                                                                Score 1850.5; DB 8;
Pred. No. 4.1e-192;
8; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "O-phosphorylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "O-phosphorylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     404
/note= "O-phosphorylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY95230 standard; protein; 405 AA
                                                                                                                                                                                                                                                                                   90.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse potassium channel TASK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                        Matches 363; Conservative
                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                              Sequence 412 AA;
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(first entry)

Wed

us-09-503-089a-5.rag

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Transmembrane potassium ion channel protein; inward potassium flux; pest control; membrane potential; pesticide; antihelminthic; nematode; insect; 2P channel; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polypeptide, a mutant potassium ion channel protein for improving inward potassium flux under acidic conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 18; Page 53; 131pp; English
                                                                                                                                                                                                                                                                 14-FEB-2001; 2001WO-US004680
                                                                                                                                                                                                                                                                                                    15-FEB-2000; 2000US-00503849
                                     Mouse 2P channel protein #1
                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-536570/59
                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAS12179
                                                                                                                                                                                      WO200161006-A2
                                                                                                                                                   Mus musculus.
                                                                                                                                                                                                                                                                                                                                       (BADI ) BASF
21-NOV-2001
                                                                                                                                                                                                                           23-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                              Pausch MH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184
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셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ,
                                                                                                                                                                                                                                                                                                                                 The present sequence is that of murine TASK (TWIK-related acid-sensitive K+ channel), a member of a new family of 2P domain potassium channels, also including human TWIK-1 (see AAY19671), human TASKI (see AAY79674) and novel human TASKI (see AAY79675). Human and mouse TASK proteins share 85% identity, indicating that they are products of orthologue genes. Host cells expressing TWIK-1 family members can be used to screen for substances that modulate the activity of members of the TWIK-1 family of potassium channels. The drugs identified may be useful in the treatment of diseases of the heart or of the nervous system, such as epilepsy, arrhythmia, vascular diseases, neurodegenerative diseases, kidney, liver or pancreas diseases, hypertension, diseases associated with ischaemia or secretion, and muscle diseases
                                                                                                                                                                                                                                             potassium transport channel, designated TASK2, useful in the treatment of hypertension or dysfunctions of the kidney, liver or pancreas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 GVGGSGFRNVYAEVLHFQSMCSCLMYKSREKLQYSIPMIIPRDLSTSDTCVEHSHSSPGG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RVVLRLKPHKAGVQWRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYALLGIPLTLV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 MFQSLGERINTLVRYLLHRAKKGLGMRRADVSMANWVLIGFFSCISTLCIGAAAFSHYEH 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 LRFMTMNAEDEKRDAEHRALLTHNGQAVGLGGLSCLSGSLGDVRPRDPVTCAAAAGGVGV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 MFOSLGERINTFVRYLLHRAKRGLGMRHAEVSMANNVLIGFVSCISTLCIGAAAFSYYER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --GGGGFRNVYAEVLHFQSMCSCLWYKSREKLQYSIPMIIPRDLSTSDTCVEQSHSSPGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 QNVRTLALIVCTFTYLLVGAAVFDALESEPELIERQRLELRQQELRARYNLSQGGYEELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LRFMTMNAEDEKRDAEHRALLTRNGOAGGGG-----GGSAHTTDTASSTAAA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 RVVLRLKPHKAGVQWRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCWFYALLGIPLTLI
                                                                                                                                                                                                                           outwardly rectifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89.1%; Score 1819; DB 3; Length 405; 88.1%; Pred. No. 1.1e-188; ive 9; Mismatches 25; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGRYSDTPSRRCLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid encoding a non-inactivating
                                                                                                                                                 Lazdunski M;
                                                                                                                                                                                                                                                                                                    Disclosure; Fig 8; 91pp; English.
                                                                                                           (CNRS ) CNRS CENT NAT RECH SCI.
                                                   98US-0107692P.
99US-00436265.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 88.1
Matches 357; Conservative
                                                                                                                                                 Lesage F,
                                                                                                                                                                                      WPI; 2000-376487/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 405 AA;
                                                    09-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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The invention relates to a mutant potassium ion channel protein, having four membrane spanning domains and two pore forming domains, comprising a mutation at the second pore forming domain. The expression of the mutant protein in a cell confers improved inward potassium flux and the ability to grow in the presence of potassium. Mutant proteins and their corresponding polynucleotide sequences can therefore be used to improve inward potassium flux into cells under acidic conditions by modularing the membrane potential using therapeutic agents. The sequences may be used to develop agonists and antagonists of potassium channel proteins in order to control pests such as nematodes and insects. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 RVVLRLKPHKAGVQWRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYALLGIPLTLV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 MFQSLGERINTLVRYLLHRAKKGLGMRRADVSMANMVLIGFFSCISTLCIGAAAFSHYEH 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VVLRFMTMNAEDEKRDAEHRALLTHNGQAVGLGGLSCLSGSLGDGVRPRDPVTCAAAA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73 RVVLRLKPHKAGVQWRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYALLGIPLTLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQYVAFSFVYILTGLTVIG--AFLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 QNVRTLALIVCTFTYLLVGAAVFDALESEPELIERQRLELRQQELRARYNLSQGGYEELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VVLRFMTMNAEDEKRDAEHRALLTRNGQAGGGG------GGSAHTTDTASSTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1235.5; DB 4
Pred. No. 2.6e-125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Mismatches
                                                                                                                                                                                                                                                                                                                           represents a mouse 2P channel protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB18807 standard; protein; 374 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                60.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 83.9
Matches 250; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 309 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB18807
ID AAB1
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AAU07620 standard; protein; 309

AAU07620;

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ELERVVLRLKPHKAGVQWRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMPYALLGIPL 120
-AEVLHFOSMCSCLWYKSREKLQYSIPMIIPRDLSTSDTCVEQSHSSPGGGGRYSDTPSR 359
                            Polypeptides and polynucleotides of the potassium channel family, useful for identifying agonists/antagonists of therapeutic use and diagnosis and treatment of cancer, pulmonary, cardiovascular, inflammatory and renal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is encoded by an expressed sequence tag (EST) which is related to a cDNA encoding a human DKCNI polypeptide. The polypeptide is a member of the potassium channel family. The DKCNI polypeptides and polynucleotides are useful for treating diseases including cancer, pulmonary, cardiovascular, inflammatory or renal diseases, pain, psychiatric disorders including depression and schizophrenia, migraine, elseperse including Alzheimer's, neurological disorders, migraine, epilepsy, sleep-related disorders, erectile dysfunction and alopecia. DKCNI polynucleotides are useful as diagnostic reagents for detecting mutations in the associated gene
                                                                                                                                                                                                                                                                                                                                                                                                            Human; DKCN1; potassium channel; cancer; pulmonary disease; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKRQNVRTLSLIVCTFTYLLVGAAVFDALESDHEMREBEKLKABEIRIKGKYNISSEDYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKRONVRTLALIVCTFTYLLVGAAVFDALESEPELIERORLELROGELRARYNLSQGGYE
                                                                                                                                                                                                                                                                                                                                                                                                                           cardiovascular disease; inflammatory disease; renal disease; pain; psychiatric disorder; schizophrenia; neurodegenerative disease; halzheimer; s disease; neurological disorder; migraine; epilepsy; sleep-related disorder; erectile dysfunction; alopecia; expressed sequence tag; EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 374;
                                                                                                                                                                                                                                                                                                                                                                  CDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Η,
                                                                                                                                                                                                                                                                                                                                                                  Protein encoded by an EST related to a human DKCN1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54.7%; Score 1116; DB 3;
59.0%; Pred. No. 3.5e-112;
ive 44; Mismatches 96;
                                                                                                                344 NSLFP----SPISSISPGLHSFTDHQRLMKRRKSV 374
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                                                                                        RCLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV
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                                                                                                                                                                                                                                         standard; protein; 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SMIK ) SMITHKLINE BEECHAM PLC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-MAR-1999; 99GB-00005061.
10-FEB-2000; 2000GB-00003112.
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                                                                                                                                                                                                                                                                                                                        (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 233; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Godden
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200053628-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                          22-JAN-2001
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                                                                                                                                                                                                                                                                                   AAB18813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polypeptides and polynucleotides of the potassium channel family, useful for identifying agonists/antagonists of therapeutic use and diagnosis and treatment of cancer, pulmonary, cardiovascular, inflammatory and renal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YEHWTFFQAYYYCFITLITIGFGDYVALQKDQALQTQPQYVAFSFVYILTGLTVIGAFLN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVVLRFWTWNAEDEKRDAEHRALLTRNGQAGGGGGGGGAHTTDTASSTAAAGGGGFRNVY 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             is a member of the potassium channel family. The DKCNI polypeptides and polymucleotides are useful for treating diseases including cancer, pulmonary, cardiovascular, inflammatory or renal diseases, pain, psychiatric disorders including depression and schizophrenia, neurodegenerative disease including Alzheimer's, neurological disorders, and angraine, epilepsy, sleep-related disorders, erectile dysfunction and alopecia, DKCNI polymucleotides are useful as diagnostic reagents for detecting mutations in the associated gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence represents human DXCN1 polypeptide. The polypeptide
                                                                                                                                    potassium channel; cancer; pulmonary disease; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CEEWSFFHAYYYCFITLTTIGFGDYVALQTKGALQKKPLYVAFSFWYILVGLTVIGAFLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKRQNVRTLSLIVCTFTYLLVGAAVFDALESDHEMREBEKLKAEEIRIKGKYNISSEDYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELERVVLRLKPHKAGVOWRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYALLGIPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22; Gaps
                                                                                                                                                     cardiovascular disease; inflammatory disease; renal disease; pain; psychiatric disorder; schizophrenia; neurodegenerative disease; Alzheimer's disease; neurological disorder; migraine; epilepsy; sleep-related disorder; erectile dysfunction; alopecia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Meadows HJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96;
                                                                                          Amino acid sequence of a human DKCN1 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 1116; DB 3;
; Pred. No. 3.5e-112;
44; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chapman CG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 25; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMIK ) SMITHKLINE BEECHAM PLC
                                                                                                                                                                                                                                                                                                                                                                                                                                    05-MAR-1999; 99GB-00005061.
10-FEB-2000; 2000GB-00003112.
                                                                                                                                                                                                                                                                                                                                                                                          02-MAR-2000; 2000WO-EP001750.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tch 54.7%;
al Similarity 59.0%;
233; Conservative 44
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                                                  (first entry)
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                                                                                                                                                                                                                                                                                                         WO200053628-A2
                                                                                                                                      Human; DKCN1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Duckworth DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                    05-MAR-1999;
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                                                  22-JAN-2001
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           AAB18807;
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of diseases associated with altered ALMD GLITTL, J. T. T. Epilepsy, diseases are cancer, brain associated disorders (such as epilepsy, Alzheimer's disease, Parkinson's disease, stroke, multiple sclerosis, migraine), psychiatric disorders (such a depression schizophrenia, bipolar diseases) and diseases related to the heart (such as arrhythmias), diseases related to pancreas (such as pancreatitis and
                                                                                                                                                  Similarity
                                                                                                          Sequence 374 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200177174-A2
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                                                                                                                                   Query Match
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                                         180
                                                                                                                                                LVVLRFWTMNAEDEKRDAEHRALLTRNGQAGGGGGGSAHTTDTASSTAAAGGGGFRNVY 300
                                                                                                                                                                           286
                                                                                                                                                                                                   -AEVLHFQSMCSCLWYKSREKLQYSIPMIIPRDLSTSDTCVEQSHSSPGGGGRYSDTPSR 359
                                                                                                                                                                                                                            287 KADVPDLÓSVCSCTCYRSQD---YGGRSVAPQNSFSAKLAPHYFHSISYKIEEISPSTLK 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      potassium channel-associated disorder; brain associated disorder; epilepsy; Alzhaimer's disease; Parkinson's disease; multiple sclerosis; migraine; psychiatric disorder; depression; schizophrenia; diabetes; bipolar disease; heart disease; arrhythmia; pancreas disease;
181 YEHWTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQYVAFSFVYILTGLTVIGAFLN
                                                                                                          181 CEEWSFFHAYYYCFITLTIGFGDYVALQTKGALQKKPLYVAFSFWYILVGLTVIGAFLN
                                      TLVMFQSLGERINTLVRYLLHRAKKGLGMRRADVSMANMVLIGFFSCISTLCIGAAAFSH
                                                                                                                                                             termed KCNB (potassium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A nucleic acid encoding a potassium channel, termed KCNB (potassi channel expressed in breast), useful in the diagnosis, prognosis treatment of diseases associated with altered KCNB activity or
                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of human potassium channel protein KCNB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         potassium channel protein; KCNB; breast tissue;
                                                                                                                                                                                                                                                                       344 NSLFP----SPISSISPGLHSFTDHORLMKRRKSV 374
                                                                                                                                                                                                                                                      RCLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394
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                                                                                                                                                                                                                                                                                                                                                 AAG63938 standard; protein; 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-MAR-2000; 2000US-0186915P
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                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                              TLVMFQSLGERINTLVRYLLHRAKKGLGMRRADVSMANMVLIGFFSCISTLCIGAAAFSH 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -AEVLHFQSMCSCLWYKSREKLQYSIPMIIPRDLSTSDTCVEQSHSSPGGGGRYSDTPSR 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                           TLVMFQSLGERMITFVRYLLKRIKKCCGMRNTDVSMENNVTVGFFSCMGTLCIGAAAFSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKRONVRTLALIVCTFTYLLVGAAVFDALESEPELIERQRLELRQQELRARYNLSQGGYE
                                                                                                                                                 ELERVVLRLKPHKAGVQWRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYALLGIPL
                                                                                                                                                                                                                                                                YEHWTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQYVAFSFVYILTGLTVIGAFLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; transporter and ion channel; TRICH; akinesia; cystic fibrosis;
                                                             Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diabetes mellitus; Parkinson's disease; myasthenia gravis; dementia; cardiac disorder; angina; hypertension; myocarditis; hyperglycaemia; neurological disorder; Alzheimer's disease; cataract; infertility; Wilson's disease; schizophrenia; Grave's disease; addison's disease; Huntington's disease; multiple sclerosis; meningitis; hypotensive; cardiant; nootropic; neuropercetive; neuroleptic; ophthalmological; cardiant; notropic)
                                                             22;
                                                             96; Indels
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225. .243
  ; Score 1116; DB 4;
; Pred. No. 3.5e-112;
44; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RCLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human transporters and ion channels (TRICH)-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= Transmembrane_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .25
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ż
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE13279 standard; protein; 374
54.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                             Matches 233; Conservative
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Human; tandem of P domains in a weak inward rectifying potassium channel; TWIK-9; 56115 protein; central nervous system disorder; sleep disorder; Alzheimer's disease; Parkinson's disease; barkinson's disease; hypertension; neuropsychiatric disorder Huntington's disease; hypertension; neuropsychiatric disorder depression; schizophrenia; effective disorder; cardiac-related disorder; learning disorder; cellular proliferation disorder; migration disorder; migration disorder; migration disorder; arteriosclerosis; gene therapy;
301 -AEVLHFQSMCSCLWYKSREKLQYSIPMIIPRDLSTSDTCVEQSHSSPGGGGRYSDTPSR 359
                         .27. .130
'note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   319. .321
/note= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Casein kinase II phosphorylation site"
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.e= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note= "Casein kinase II phosphorylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "Mature human TWIK-9 protein"
                                                                                                                    344 NSLFP----SPISSISPGLHSFTDHORLMKRRKSV 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9. .26
/note= "Transmembrane domain 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108. 125
//note= "Transmembrane domain 2"
117. 122
/note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Transmembrane domain 4" 236. .241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "Transmembrane domain 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "N-myristoylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "N-glycosylation site"
                                                                                   360 RCLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amnesia; pain disorder; cancer; prophylaxis
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/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                               AAE22989 standard; protein; 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "P-loop"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "P-loop"
                                                                                                                                                                                                                                                                                                                 21-AUG-2002 (first entry)
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/note= "E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to human transporters and ion channels (TRICH) and the polynuclectides encoding them. The composition comprising TRICH or agonist of TRICH is useful for treating a disease or condition associated with decreased expression of functional TRICH or condition associated with overexpression of TRICH respectively. The composition comprising Above a useful for diagnosing a condition of disease associated with expression of TRICH in a subject, where the disorders include a transport disorder such as akinesia, cystic fibrosis, diabetes mellitus, cardiacon's disease, myasthenia gravis, cardiac disorders associated with transport e.g. Alzheimer's disease, Wilson's disease, consistent of a sandia, hypertension, myocarditis, neurological disorders associated with transport e.g. Alzheimer's disease, Wilson's disease, contizophrenia, cataracts, infertility, hyperglycaemia, Grave's disease, dementia, multiple contire, addison's disease, Huntington's disease, dementia, multiple contire, addison's disease, Huntington's disease, dementia, multiple contire, addison's disease, Huntington's disease, dementia, multiple content entering a transcript image of a tissue or cell type, which represents the global pattern of gene expression by a particular tissue or cell type and for analysing the proteome of a tissue or cell type.

The global pattern of gene expression by a particular tissue or cell type and for analysing the proteome of a tissue or cell type.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 YEHWTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQYVAFSFVYILTGLTVIGAFLN 240
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                                                                                                                                                                                                                                                                        Reddy R, Thornton M, Borowsky ML, Tang YT, Khan FA, Tribouley CM; Gandhi AR, Yao MG, Sanjanwala MS, Baughn MR, Nguyen DB, Policky JL; Yue H, Seilhamer JJ, Walia NK, Lal P, Kearney L, Walsh RT, Lu DAM; Lu Y, Greene BD, Raumann BE, Patterson C;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Polypeptides of human transporters and ion channels, useful for diagnosing, treating or preventing disorders of transport, neurological, muscle, immunological and cell proliferative disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 124-125; 150pp; English.
                                                                                                                            20-APR-2000; 2000US-0199020P.
28-APR-2000; 2000US-0200552P.
05-MAY-2000; 2000US-020348P.
                                               06-APR-2001; 2001WO-US011206.
                                                                                     2000US-0195595P.
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                                                                                                                                                                                                                                   (INCY-) INCYTE GENOMICS INC.
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Best Local Similarity 59.0%
Matches 233; Conservative
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N-PSDB; AAD21998.
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                                                                                     06-APR-2000;
12-APR-2000;
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Gandhi AR,
      18-OCT-2001
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-AEVLHFQSMCSCLWYKSREKLQYSIPMIIPRDLSTSDTCVEQSHSSPGGGGRYSDTPSR 359
                                                                               Human; TWIK-9; ion channel family; ICF; cancer; leukaemia; Alzheimer's disease; Parkinson's disease; multiple sclerosis; epilopsy; hepatic disorder; cardiovascular disorder; cytostatic; neuroprotective; nootropic; antiparkinsonian; hepatotropic; cardiovascular.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9, alpha2delta-4, 54414, or 53763 nucleic acids and proteins, useful for preventing, disgnosing and treating e.g. cancers, Alzheimer's disease cardiovascular disorders.
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                                                                                                                                                          344 NSLFP----SPISSISPGLHSFTDHQRLMKRRKSV 374
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2000US-0185938P.
2000US-0195734P.
2000US-0195993P.
2000US-0199799P.
2000US-0233537P.
2000US-0235059P.
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2000US-0256588P.
2000US-0258028P.
2001US-00796720.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-MAY-2002; 2002US-00146733
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                                                                                                                                                                                                                                                                                                                                                                                  Human TWIK-9 protein.
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25-SEP-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to human tandem of P domains in a weak inward rectifying potassium channel polypeptides (TWIK-9) termed 56115 and nucleic acid molecules encoding such polypeptides. Sequences of the invention are useful for treating TWIK-9-associated or related disorders invention are useful for treating TWIK-9-associated or related disorders such as central nervous system disorders (e.g. Alzheimer's disease, autonomic function disorders (e.g. parkinson's disease), autonomic function disorders (e.g. phpolar affective disorders, neuropsychiatric disorders (e.g. depression, schizophrenia), learning or memory disorders (e.g. amnesia), cipipolar affective disorders, cardiac-related disorders (e.g. arteriosclerosis, myocardial infarction), pain disorders (e.g. cancer) and disorders of tissues in which TWIK-9 protein is predominantly expressed. They are also useful in screening assays, detection assays (e.g. chromosomal mapping, tissue typing, forensic biology), predictive medicine (e.g., diagnostic assays, prognostic assays, monitoring clinical trials and pharmacogenomics) and in methods of treatment (e.g. therapeutic and prophylactic). TWIK-9 polymucleotides are used in gene therapy. The present sequence is human TWIK-9 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated human tandem of P domains in weak inward rectifying potassium channel polypeptide, 56115, useful for treating central n system, cardiovascular, pain, and cellular proliferation disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22;
                     /note= "Protein kinase C phosphorylation site"
341. .343
/note= "Protein kinase C phosphorylation site"
                                                                                                                                    dependent protein kinase
                                                                                                 site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.7%; Score 1116; DB 5; Length 374; 59.0%; Pred. No. 3.5e-112; ive 44; Mismatches 96; Indels 2;
.333
== "Protein kinase C phosphorylation
                                                                           360. .363
/note= "Casein kinase II phosphorylation
370. .373
                                                                                                                                    CGMP
                                                                                                                                                        phosphorylation site
                                                                                                                                    and
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                                                                                                                                    note= "cAMP
                                                                                                                                                                                                                                                                     25-SEP-2001; 2001WO-US030048.
                                                                                                                                                                                                                                                                                                         25-SEP-2000; 2000US-0235059P
                                                                                                                                                                                                                                                                                                                                             (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 59.0
Matches 233; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          2002-416481/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAD36247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 374 AA;
                                                                                                                                                                                            WO200226983-A2
 Modified-site
                                     Modified-site
                                                                           Modified-site
                                                                                                                 Modified-site
                                                                                                                                                                                                                                04-APR-2002
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Best Local S
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TWIK-8, IC47611, IC47615, HNWDA-1, TWIK-9, alpha-2delta-4, 54414 and 53763 ICF nucleic acids and proteins may be used for preventing, adagnosing and treating ICF-related diseases. The sequences may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of ICF proteins by expressing inactive proteins or to supplement the production of ICF proteins. The proteins may also be used as antigens in the production of antibodies against ICF proteins and in antigens in the production of antibodies against ICF proteins and in anti-protein antibodies, against ICF protein and activity. The anti-protein antibodies against ICF protein antibodies may be used to regulate ICF protein expression and activity. The antibodies may be used to regulate ICF protein expression and activity. The antibodies may be used to prevent, diagnose and treat a wide variety of disorders, e.g. cancers and leukaemia, Alzheimer's disease, Parkinson's disease, multiple scherosis, epilepsy, hepatic disorders and cardiovascular disorders. The sequence tepresents the human TWIK-9 protein of the invention. Note: The sequence data for this parent is also available in electronic format from USPTO at seqdata.uspto.gov/sequence.html.
                 $$$$$$$$$$$$$$$$$$$$$$$$
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Sequence 374 AA;

Ŋ, 120 180 240 240 286 ELERVVLRLKPHKAGVQWRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYALLGIPL 120 TLVMFQSLGERINTLVRYLLHRAKKGLGMRRADVSMANMVLIGFFSCISTLCIGAAAFSH 180 LVVLRFWTWNAEDEKRDAEHRALLTRNGQAGGGGGGSAHTTDTASSTAAAGGGGFRNVY 300 301 -AEVLHFQSMCSCLWYKSREKLQYSIPMIIPRDLSTSDTCVEQSHSSPGGGGRYSDTPSR 359 287 KADVPDLQSVCSCTCYRSQD---YGGRSVAPQNSFSAKLAPHYFHSISYKIEEISPSTLK 343 121 TLVMFQSLGERMNTFVRYLLKRIKKCCGMRNTDVSMENWTVGFFSCMGTLCIGAAAFSQ MKRQNVRTLALIVCTFTYLLVGAAVFDALESEPELIERORLELROOELRARYNLSOGGYE 96; Indels 22; Gaps Query Match 54.7%; Score 1116; DB 8; Length 374; Best Local Similarity 59.0%; Pred. No. 3.5e-112; Matches 233; Conservative 44; Mismatches 96; Indels 2: 344 NSLFP----SPISSISPGLHSFTDHQRLMKRRKSV 374 360 RCLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394 121 241 61 61 g ò 셤 è g 8 8 ò a ઠે a ò ઠે

Search completed: July 13, 2005, 08:39:50 Job time : 100.204 secs

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GenCore version 5.1.6

Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on:
July 13, 2005, 08:02:40 ; Search time 20.7368 Seconds

(without alignments)

1828.118 Million cell updates/sec
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Title:
US-09-503-089A-5
Perfect score: 2042
Sequence: 1 MKRQNVRTLALIVCTFTYLL......STGLHSLSTFRGLMKRRSSV 394
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database: PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

hypothetical prote probable potassium inward rectifier p hypothetical prote hypothetical prote protein T12C9.3 [i TASK-5 protein - h probable potassium hypothetical prote potassium channel hypothetical prote hypothetical prote hypothetical prote prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote probable potassium probable potassium hypothetical prote prote prote prote potassium channel potassium channel outward rectifier potassium channel f22b7.7 protein hypothetical hypothetical hypothetical Description SUMMARIES JC7703 T43509 T32347 T19860 T43361 S6556 T28933 T25392 T123907 T30037 S44635 T27681 T23182 T43364 T43363 T43531 T26229 T45032 T27550 T43393 T13807 Query Match Length 443 1001 335 427 244 239.5 235.5 234.5 231.5 Result

hypothetical prote	potassium channel	hypothetical prote	potassium channel	hypothetical prote	hypothetical prote	hypothetical prote	_							
T16629	T43394	T24626	T15178	T26616	T23700	T22269	T26953	T21683	T16426	T43357	T27364	T21551	T23373	T23746
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519	461	009	350	643	539	504	1136	586	551	555	700	099	523	383
11.3	11.2	10.9	10.6	10.6	10.3	10.3	10.3	10.1	9.9	9.9	9.6	9.6	9.5	9.3
231.5	229	222.5	216	215.5	211	210.5	210	205.5	201.5	201.5	200.5	199.5	193.5	190.5
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A/Accession: JC7703
C/Comment: This protein, a new member of the tandem-pore K+ channel family with four tr
C/Comment: This protein, but does not produce a functional plasma membrane K+ current by itse
C/Genetics:
A/Gene: task-5
A/Amap position: 20q12
C/CYMORAIN: transmembrane protein
F/107-128/Domain: transmembrane segment #status predicted <TMS1>
F/107-128/Domain: hydrophobic cytoplasmic linker #status predicted
F/156-180/Domain: transmembrane segment #status predicted <TMS3>
F/156-180/Domain: transmembrane segment #status predicted <TMS3>
F/156-180/Domain: transmembrane segment #status predicted <TMS3>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C;Accession: JC7703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELERVVLRLKPHKAGVQWRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYALLGIPL
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                                                                                                                Rikim, D.; Gnatenco, C. Babchen. 284, 923-930, 2001
Blochen. Blophys. Res. Commun. 284, 923-930, 2001
A;Hitle: TASK-5, a new member of the tandem-pore K+ channel family.
A;Reference number: JC7703; MUID:21303050; PMID:11409881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
41.4%; Score 846; DB 2; Length 330;
Best Local Similarity 64.7%; Pred. No. 1e-68;
Matches 167; Conservative 32; Mismatches 59; Indels
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LVVLRFLVASADWPERAA 258
TASK-5 protein - human
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C;Species: Genorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T19860
C;Accession: T19860
C;Accession: T19860
A;Reference number: Z19188
A;Accession: T19860
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Actession: T19860
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-334 <WIL>
A;Residues: 1-334 <WIL>
C;Censerios: EMBL:Z70266; PIDN:CAA94204.1; GSPDB:GN00028; CESP:C40C9.1
A;Experimental source: clone C40C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Introns: 34/1; 60/2; 98/1; 145/3; 160/3; 181/1; 204/1; 252/2; 279/2; 306/3
                                    LIVIGAPLNLVVLRFMIMNAEDEKRDAEHRAL----LIRNGQAGGGGGGSAHTTDTASS
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                                                                                                                    114 ALLGIPLTLVMFQSLGERINTLVRYLLHRAKKGLGMRRADVSMANMVLIGFFSCISTLCI
                                                                                                                                                   174 --GAAAFSHYEHWIFFQAYYYCFITLITIGFGDYVALQKDQALQTQPQYVAFSFVYILTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           288 TAAAAGGGGFRNVYAEVLHFQSMCSCLWYKSREKLQYSIPMIIPRDLSTSDTCVEQSHSSP
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; Pred. No. 2.3e-46;
46; Mismatches 81;
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Best Local Similarity
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A; Map position: X
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C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Date: 29-Oct-1999 #sequence Oct.
C;Date: 29-Oct-1999 #sequence Oct.
C;Date: 29-Oct-1999 #sequence Oct.
C;Date: 29-Oct-1999 #text_change 09-Jul-2004
C;Date: 29-Oct-1999
C;Date: 29-Oct-1999 #text_change 09-Jul-2004
C;Date: 29-Oct-1999
C;Date: 29-Oct-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ELERVVLRLKPHKAGVQWRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYALLGIPL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TLVMFQSLGERINTLVRYLLHRAKKGLGMRRADVSMANMVLIGFFSCISTLCI--GAAAF 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178 SSYENWIYFDAVYYCFVTLTTIGFGDYVALOKRGSLOTQPEYVFFSLVFILFGLTVISAA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INLVVLRFWTWNAEDEKRDAEHRAL----LTRNGQAGGGGGGGAHTTDTASSTAAAGGG 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   outward rectifier potassium channel homolog twk-23 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
                                                                Species: Caenorhabditis elegans
Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SHYEHWTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQYVAFSFVYILTGLTVIGAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKRONVRTLALIVCTFTYLLVGAAVFDALESEPELIE-----RORLELRQOELRARYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKRONVRTLALIVCTFTYLLVGAAVFDALESEPELIERQRLELRQQELRARYNLSQGGYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GFRNVYAEVLHPQSMCSCLWYKSREKLQYSIPMIIPRDLSTSDTCVEQSHSSPGGG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                           probable potassium channel chain n2P38 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-C;Accession: T43509
R;Wang, Z.W.; Salkoff, L.
submitted to the EMBL Data Library, August 1998
A;Description: Potassium channels in C. elegans.
A;Reference number: Z22450
A;Accession: T43509
A;Accession: T43509
A;Accession: T43509
A;Residues: 1-329 < *WAN's
A;Molecule type: mRNA
A;Residues: 1-329 < *WAN's
A;Cross-references: UNIPROT:017185; EMBL:AF083652; PIDN:AAC32863.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 40.2%; Score 820; DB 2; Best Local Similarity 48.3%; Pred. No. 2.2e-66; Matches 172; Conservative 54; Mismatches 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39.5%; Score 806.5; DB 2
47.4%; Pred. No. 3.8e-65;
tive 54; Mismatches 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 47.4%;
Matches 172; Conservative 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene: twk-23; CESP:F34D6.3
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A;Introns: 12/3; 54/3; 90/3; 158/1; 173/1; 227/3; 299/3; 346/2; 378/2; 405/1; 452/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               338 AYIIFGLSLATMCIDLAGTEYIRKIHYLGTKWEDAK------GAVWIGLQAGEH 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTTDTASSTAAAGGGGFRNVYAEVLHFQ----SMCSCLWYKSREKLQYSIPM----- 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          386 LLKHTGIEVIKTAGGKLVQVRGAVLSSKEARELGMSYLLQFNYQHKNVLYEPLTGNLAKV 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:U64598; PIDN:AAC47976.1; GSPDB:GN00028; CESP:C52B9.6
A;Experimental source: strain Bristol N2; clone C52B9
                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein C52B9.6 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: T28933 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000 C;Accession: T28933 #sequence_revision 1996 A;Nelson, J. submitted to the EMBL Data Library, July 1996 A;Description: The sequence of C. elegans cosmid C52B9. A;Reference number: Z20545 A;Accession: T28933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein T28A8.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Bate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T25392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 VKNMFQAYRNQFITAKHLLNKTREDEVLWTFPNSMFFAATVITTIVQVKNRSGNRVVFSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GYGHAAPSTDGGKVFCMFYALLGIPLTLVMFQSLGERINTLVRYLLHRAKKGLGMR----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        226 VYILTGLTVIGAFLNLV-----VLRFMTMNAEDEKRDAEHRALLTRNGQAGGGGGGSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 LALIVCTFTYLLVGAAVFDALESEPEL-----IERQRLELRQQELRARYNLSQGGYEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 307.5; DB 2; Length 513;
Pred. No. 9.1e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                    255 LGLIAMLAVLETFCELHELKKFRKMFYVKKDKDEDQVH 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.1%; Score 307.5; DB 2; 23.6%; Pred. No. 9.1e-20; ive 56; Mismatches 139;
                                                                            ---LTVIGAFLNLVVL---RFMTMNAEDEKRDAEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Reference number: Z20027
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Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-513 <NEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Gene: CESP: C52B9.6
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C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: 365566
C;Accession: 365566
A;Title: TWIK-1, a ubiquitous human weakly inward rectifying K(+) channel with a novel 6
A;Title: TWIK-1, a ubiquitous human weakly inward rectifying K(+) channel with a novel 6
A;Reference number: 865566
A;Reference number: 865566; MUID:96183184; PMID:8605869
A;Accession: 56556
A;Accession: 56556
A;Accession: 26556
A;Extus: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-336 <LES>
A;Cross-references: UNIPROT:000180; EMBL:U33632; NID:gl086490; PIDN:AAB01688.1; PID:gl08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86 SNYGVSVLSNASGNWNWDFTSALFPASTVLSTTGYGHTVPLSDGGKAFCIIYSVIGIPFT 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 AAFSHYEHWTPFQAYYYCPITLTTIGFGDYVALQKDQALQTQPQYVAFSFVYILTGLTVI 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200 AAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQKFREL----YKIGITCYLL 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 MFQSLGERINTLVRYLLHRAKKGLGMR----RADVSMANMVL---IGFFSCISTLCIGA 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 ONVRTLALIVCTFTYLLVGAAVFDALESEPELIERQRLELRQQELRARYNLSQGGYEELE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 LIVCTFTYLLVGAAVFDALESEPELIERQRL-ELRQQELRARYNLSQGGYEELERVVLRL 69
Species: Caenorhabditis elegans
| Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
| Accession: T43361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inward rectifier potassium channel TWIK-1 - human
C;Species: Homo sapiens (man)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S65566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: UNIPROT: 076790; EMBL: AF083646; PIDN: AAC32857.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29.3%; Score 599; DB 2; Length 364; 46.1%; Pred. No. 2.5e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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          C;Species: Caenorhabditis elegans
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #tes
C;Accession: T4336f, L.
R;Wang, Z;W. Salkoff, L.
R;Wang, Z;W. Salkoff, L.
Submitted to the EMBL Data Library, August 1998
A;Pescription: Potassium channels in C. elegans.
A;Reference number: Z22450
A;Accession: T43361
A;Reference preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-364 <WAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Pred. No. 2.5e-
46; Mismatches
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Matches 119; Conservative
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A;Cross-references: UNIPROT:021729; EMBL:274475; PIDN:CAA98957.1; GSPDB:GN00023; CESP:RCA,Experimental source: clone R04F11
                                                                                                                                                                                               198 CCWIRLPRRHIPMPTLELLORIOKLYPNNNNPTVAATAASAGGGTGRRKKQQRDNVSDAG 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----RADVSMANMVLIGFFSCISTLCIG 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175 AAAFSHYEHWTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQYVAFSFVYILTGLTV 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein R04F11.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C;Accession: T23907 B;Harris, B submitted to the EMBL Data Library, June 1996 A;Reference number: Z19816 A;Reference number: Z19816 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Residues: DNA A;Residues: 1-524 <WILL)
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hypothetical protein F20Al.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53 NLSQGGYEELERVVL----RLKPH-----KAGVQWRFAGSFYFAITVITTIGYGHAAP
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                                                                  18 LVLLSIGYTLIGALCFHHYEKPYEQQLRNETSRRIGELKNRVMDQLWRMSNNGTAYSTWR
                                                                                                                                                    ----VLIGFFSCISTLCIGAAAFSHYEHWTFFQAYYYCFITLTTIGFGD
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A;Introns: 35/3; 83/2; 131/1; 170/1; 261/1; 306/1; 338/1; 369/1; 489/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102 STDGGKVFCMFYALLGIPLTLVMFQSLGERINTLV------------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92; Indels 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 524;
                                                                                                                                                                                                                                                                                  205 YVALQKDQALQTQPQYVAFSFVYILTGLTVIGAFLNLVVLRFM 247
                                                                                                                                                                                                                                                                                                                   489 IVPENHD------YIAIMLIYLGVGLSVTTMCIDLAGIQYI 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 LIVCTPTYLLVGAAVFDALESEPELIERQRLELRQOELRARY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.5%; Score 275; DB 2; 23.9%; Pred. No. 8.2e-17; ive 38; Mismatches 92.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------RY-----LLHRAKK-----
                             119 PLTLVMFQSLGERINTLVRYLLHRAKKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 -----
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Best Local Similarity 23.9%
Matches 88; Conservative
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                                                                                                                                                        156 MANM-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: CESP: R04F11.4
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Science 282, 2012-2018, 1998

A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: AF500, MUID:199068613; PMID:3851916

A;Note: see websites genome.wustl.edu/gsc/C elegans/ and www sanger.ac.uk/Projects/C ele A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Status: preliminary

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1910 <STO>

A;Cross-references: GB:chr_I; PIDN:AC71141.1; PID:g1086770; GSPDB:GN00020; CESP:T12C9.3

A;Genetics:
A;Gen
A,Accession: T25392
A,Stetues prelimary; translated from GB/EMBL/DDBJ
A,Stetues prelimary; translated from GB/EMBL/DDBJ
A,Holecule type: DNA
A,Residues: 1-393 <WIL>
A,Cross-references: UNIPROT: Q3XU07; EMBL: Z92813; PIDN: CAB07286.1; GSPDB: GN00021; CESP:TZ
A,Experimental source: clone T28A8
C,Genetics:
A,Gene: CESP:T28A8.1
A,Gene: CESP:T28A8.1
A,Map position: 3
A,Map position: 3
A,Introns: 73/1; 112/3; 179/2; 209/3; 287/2; 310/3; 364/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :: ||| :
249 INNNEKEVWKEDIEKELMLYSEKLYKAFKEQYVRYSDVRTIGFEGRSSYEEADETGGDSE 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RLKPHKAG------VOWRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYALLGI 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein T12C9.3 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: H88124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 -AKKGLGMRRADVS---MANWVLIGFFSCI----STLCIGAAAFSHYEHWTFFQAYYYCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 QNVRTLA-----LIVCTFTYLLVGAAVFDALES--EPELIERQRLELRQQELRARYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 VSLÍVLSVVÝVGFGAFLFYQLEQPNEVEVRARNÍERFNÍHKRÓMIEHLWEMRESGIGOHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -QELRARY--NLSQGGYEELERVVLRLKPHKAG-----VQWRFAGSFYFAITVITTIGYG
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                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   195 ITLTTIGFGDYVALQKDQALQTQPQYVAFSFVYILTGLTVIGAFLNLVVLRFM 247
                                                                                                                                                                                                                                                                                                                                                                                                                   62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107;
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                                                                                                                                                                                                                                                                                                                                                    Length 393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                 Query Match 14.3%; Score 293; DB 2; Length 39 Best Local Similarity 26.6%; Pred. No. 1.4e-18; Matches 78; Conservative 57; Mismatches 96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 LALIVCTFTYLLVGAAVFDALESEPEL----IERQRLELRQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49; Mismatches 107;
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Best Local Similarity 23.3
Matches 80; Conservative
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101

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C;Species: Drosophila melanogaster
C;Date: 11-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T13807
C;Accession: T1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             193 EMKEJERQERHDLDIFDLPLPVGIALIVTWIFICSFVLSVWDHNWTLLESFYFFFTSLST 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77 KGNTSQRLTTFFIEELGSYEN----QLGVKWSQQKMDWDFWNAVLFAGTICTTIGYGHIY 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200 IGFGDYVALQKDQALQTQPQYVAFSFVYILTGLTVIGAFLNLVVLRFMT---MNAEDEKR 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 KVFCMFYALLGIPLTLVMFQSLGERINTLVRYLLHRAKK-----GLGMRRADVSMANMVL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162 IGFFSCIST-LCIGAAAFSHYEHWTFFQAYYYCFITLTTIGFGDYV-ALQKDQALQTQPQ 219
                                                                                                                 -----GSYEELERVVLRLKPHKAGVQWRFAGSFYFAITVITTIGYGHAA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :| || | :: : || || || 253 VGLGDLV-----PSSPRILITMFGFILVGLSLVSMVINLLQAKMKSTYEAGRNDEKT 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28
17 LIIVFLIYCISGGLVFWLIEEPYQSELRDAWQHKIENNRTARVDAMMKKIFNNSDYLIYI
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                                                                                                                                                                                                                                                                 101 PSTDGGKVFCMFYALLGIPLTLVMFQSLGERINTLVRYLLHRAKKGL-----
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12.8%; Score 261.5; DB 2; Length
Best Local Similarity 25.0%; Pred. No. 3e-15;
Matches 69; Conservative 65; Mismatches 107; Indels
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FVVYQIFVIVWFIFSLGYL--VMIMTFITRGLQSKK 272
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224635
f2247.7 protein - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
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A;Gene: ORK1
A;Cross-references: FlyBase:FBgn0017561
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T21598
R;Mortimore, B.
Submitted to the EMBL Data Library, March 1997
A;Reference number: Z19447
A;Reference number: Z19447
A;Reference number: T21598
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Recission: T21598
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-443 < WIL>
A;Residues: 1-43 < WIL>
A;Residues: Caenerices: UNIPROT:045422; EMBL:292832; PIDN:CAB07375.1; GSPDB:GN00023; CESP:F3
A;Experimental source: clone F31D4
C;Genetics:
A;Gene: CESP:F31D4.7
A;Map position: 5
A;Introns: 13/3; 90/2; 149/1; 222/3; 290/3
                                                                                                                                            A,Accession: T30037
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Redicus: 1-1539 «GAT»
A,Cross-references: UNIPROT:019611; EMBL:US3150; PIDN:AAA96127.1; GSPDB:GN00023; CESP:FZ
A,Experimental source: strain Bristol N2; clone F20Al
C,Genetics: A,Genetics: B,SP,F20Al.7
A,Map position: 5
A,Introns: 19/3; 41/2; 71/2; 110/3; 135/2; 190/1; 246/1; 287/3; 491/3; 598/2; 983/2; 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148 EERWKHAILKPE-EDIGLEEPVIETVWTFWASFLYAGTIFTTIGYGNIACKTRAGQIATM 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | | :|||: ||| || ||
207 VYAFVGIPIMLVMLTSLNNFLLKWIKLITNGVSDMTLYIGVRLGITVIRQDBVQKRLRYT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172 CIGAAAFSHYEHWTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQYVAFSFVYILTG 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        327 ILSAAVFCLFEDWTFTSFYFCFISLTTIGLGD------VTPANPEYMIATFGVVIVG 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 YEBLERVVLRLKPHKAGVQ------WRFAGSFYFAITVITTIGYGHAAPSIDGGKVFCM 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LTVIGAFLNLVVLRFMTWNAEDEKRDAEHRALLTRNGQAGGGGGGSAHTTDTASSTAAA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---NTLVRYLL--HRAKKGLGMRRADVSMANM---------VLIGFFSCISTL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            379 LSMLTVCIDVLQEKLAQMYM-----ALLQKLLTEYMEAVKSG-----DPNAASAMMA 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 TLALIVCTFTYLLVGAAVFDALESEPELIERQ------RLELRQQELRA-RYNLSQGG 58
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13.1%; Score 268; DB 2; Length 1539;
Best Local Similarity 24.6%; Pred. No. 1.3e-15;
Matches 96; Conservative 60; Mismatches 126; Indels 108; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 LIVCTFTYLLVGAAVFDALES--EPEL-----IERQRLELRQQELRARYNLSQ----
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   R;Gattung, S.; Wu, X. Bata Library, March 1996 abubmitted to the BMBL Data Library, March 1996 A;Bescription: The sequence of C. elegans cosmid F20Al. A;Reference number: Z20726
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Rythomas, Ti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79 GKFLSEHLVWLYGNYLKLKYLILSRHRKERREHVCEHCHSHGMGHDMNIEEKRIPAFLVL 138
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C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004 C;Accession: S44635 R;Anderson; K.
R;Anderson; K.
aubmitted to the EMBL Data Library, March 1993 A;Description: Sequence of the C. elegans cosmid F22B7.
A;Reference number: S44628 A;Accession: S44638 A;Accession: S4628 A;A
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.pspecies: Caenorhabditis elegans
.pste: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
.hccession: T27681
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A;Map position: 2
A;Introns: 51/3; 123/1; 212/1; 261/2; 331/3; 365/1; 394/2; 414/3
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Copyright (c) 1993 - 2005. Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		di			SUMMARIES		
Result No.	Score	Query Match	Query Match Length DB	DB	ΙD	Description	
-	2042	!		6	US-09-939-484-4	Sequence 4, Appli	
7	2042	100.0	394	თ	US-09-939-483-4	Sequence 4, Appli	
٣	2042			σ	US-09-798-584-15	Sequence 15, Appl	
4	2042			14	US-10-146-733-17	Sequence 17, Appl	
S	2042			14	US-10-146-733-18	Sequence 18, Appl	
9	2042			14	US-10-146-733-8	Sequence 8, Appli	
7	1850.5			14	US-10-146-733-9	Sequence 9, Appli	
80	1819			σ	US-09-939-484-5	Sequence 5, Appli	
6	1819			σ	US-09-939-483-5	Sequence 5, Appli	
10	1278			δ	US-09-746-491-61	Sequence 61, Appl	
11	1224			8	US-08-816-011-55	Sequence 55, Appl	

Sequence 55, Appl	1:	e 41	Ÿ	194	19	60,	59,	e 42, p	19	13	'n	58	e 191	76,	N	e 2,	E,	34	e 5	6 5	Sequence 8, Appli	ω,	ý,	8, A	129	20,	4 5,	e 45	2, Aŗ	•	83,	Sequence 2, Appli		
17 US-10-870-492-55	US-09-798-584-1	4 US	15 US-10-257-022-6	US-10-074	5 US-10-074-978A-19	US-09-746-	2	15 US-10-173-999-42	-10-074-978A-1	US-10-074	US-10-146	9 US-09-746-491-58	0-074-978A-	US-10-336-472-	9 US-09-746-491-22	14 US-10-146-733-2	15 US-10-257-022-13	9 US-09-864-761-34389	4-978A-	US-10-42	US-09-939	US-09-939	9 US-09-828-746-6	6 US-10-343	7 US-10-461-862-	US-10-349-528-2	3 US-08-816-011-45	7 US-10-87	9 US-09-828-746-2		-10-1	-10-745-210-	ALIGNMENTS	
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RESULT 1

US-09-939-484-4

| US-09-939-484-4
| Sequence 4, Application US/09939484
| Sequence 4, Application US/09939484
| Sequence 4, Application US/09939484
| Sequence 4, Application US/090322A1
| GENERAL INFORMATION:
| APPLICANT: Desage, Florian |
| APPLICANT: Lesage, Florian |
| APPLICANT: Fink, Michel |
| APPLICANT: Fink, Michel |
| APPLICANT: Lazdunski, Michel |
| TITLE OF INVERTION: PAMILY OF MAMALIAN POTASSIUM CHANNELS, THEIR CONTING OF DRUGS |
| TITLE OF INVERTION: ADDITS: US/09/939,484 |
| CURRENT APPLICANTON NUMBER: US/09/939,484 |
| PRIOR APPLICANTON NUMBER: 08/14,914 |
| PRIOR PILING DATE: 1996-09-01 |
| PRIOR PILING DATE: 1996-09-04 |
| PRIOR PILING DATE: 1996-08-04 |
| PRIOR APPLICANTON NUMBER: FR 96/01565 |
| NUMBER OF SEQ ID NOS: 2.0 |
| SEQ ID NO 4 |
| LENGTH: 394 |
| TYPE: RPT |
| ORGANISM: Homo sapiens |
| PEATURE: |
| ORGANISM: Homo sapiens |
| PEATURE: |
| OCHER INCORMATION: TASK |
| US-09-39-484-4 |
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APPLICANT: Mu, David
APPLICANT: Mu, David
APPLICANT: Fowers, Scott
APPLICANT: Tularik Inc.
TITLE OF INVENTION: KCNB: A No. US20020102676Alel Potassium Channel Protein
FILE REFERENCE: 018781-004010US
CURRENT APPLICATION NUMBER: US/09/798,584
CURRENT FILING DATE: 2001-03-03
PRIOR APPLICATION NUMBER: US 60/186,951
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 2042; DB 9; Best Local Similarity 100.0%; Pred. No. 1.4e-180; Matches 394; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                               CLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
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Sequence 100 US 020020094558A1
September 100 US 020020094558A1
September 100 US 020020094558A1
September 100 US 02002009458A1
September 100 US 02002009483
September 100 US 02002009483
September 120020097939,483
SEPTEMBER PRINGE DATE: 12002009
SURENT APPLICATION NUMBER: 05/09/939,483
SURENT APPLICATION NUMBER: 05/09/144,914
PRIOR FILING DATE: 1998-09-01
SPRIOR FILING DATE: 1998-09-01
SPRIOR FILING DATE: 1998-11-15
SPRIOR PRILING DATE: 1998-11-15
SPRIOR PRILING DATE: 1998-08-04
SPRIOR FILING DATE: 1998-08-08-04
SPRIOR FILING DATE: 1998-08-08-04
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                                                                                       1 MKRQNVRTLALIVCTFTYLLVGAAVFDALESEPELIERQRLELRQQELRARYNLSQGGYE
                                                                                                                                                                                                                                                                                                                     YEHWIFFQAYYYCFITLITIGFGDYVALQKDQALQTQPQYVAFSFVYILIGLTVIGAFLN
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100.0%; Pred. No. 1.4e-180;
ive 0; Mismatches 0;
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      0; Mismatches
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Matches 394; Conservative
         394; Conservative
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US-09-939-483-4
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| APPLICANT: CULTIS, ROY A.J.
| APPLICANT: CULTIS, ROY A.J.
| APPLICANT: Gluckemann, Maria A.
| TITLE OF INVENTION: NOUSE THEREFOR |
| TITLE OF INVENTION: HWDDA.1, THEREFOR |
| TITLE OF INVENTION: MARIA 248 | MARIA 248 |
| TITLE OF INVENTION: MARIA 248 | MARIA 248 |
| TITLE OF INVENTION: NOUNER: US 60/18, 938 |
| RRIOR PLICANTON NUMBER: US 60/18, 938 |
| RRIOR PLICANTON NUMBER: US 60/199, 739 |
| RRIOR PLICANTON NUMBER: US 60/23, 018 |
| RRIOR PLICANTON NUMBER: US 60/23, 018 |
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| RRIOR PLICANTON NUMBER: US 60/25, 240 |
| RRIOR PLICANTON NUMBER: US 60/25, 240 |
| RRIOR PLICANTON NUMBER: US 60/25, 240 |
| RRIOR PLICANTON NUMBER: US 60/25, 308 |
| RRIOR PLICANTON NUMBER: US 
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                                                      1 MKRQNVRTLALIVCTFTYLLVGAAVFDALESEPELIERQRLELRQQELRARYNLSQGGYE
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   1 MKRONVRTLALIVCTFTYLLVGAAVFDALESEPELIERQRLELRQQELRARYNLSQGGYE
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US-10-146-733-18
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                                                                                                                                                                                                                                                                                            | Sequence 17, Application Us/10146733 |
| Sequence 17, Application No. Us2030316589111 |
| APPLICANT: Gluckomann, Maria A. APLICANT: MIND-11, TWIK-5, APLICANT: Gluckomann, Maria A. APLICANT: MIND-11, TWIK-5, APLICANT: Gluckomann, Maria A. APLICANTON NOWER: Us/10/146,733 |
| CURRENT FILING DATE: 2000-02-29 |
| PRIOR PALLCANTON MARIER: US 60/195,734 |
| PRIOR PALLCANTON MARIER: US 60/195,730 |
| PRIOR PALLCANTON MARIER: US 60/196,730 |
| PRIOR PALLCANTON MARIER: US 60/196,73
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   301 AEVLHFQSMCSCLWYKSREKLQYSIPMIIPRDLSTSDTCVEQSHSSPGGGGRYSDTPSRR 360
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                                                                        361 CLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394
                                                                                                         361 CLCSGAPRSAISSVSTGLHSLISTFRGLMKRRSSV 394
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
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ORGANISM: Homo sapiens
US-10-146-733-17
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Sequence 8, Application US/10146733

Publication No. US20030165891A1

GENERAL INFORMATION:

APPLICANT: CUttis, Nory A.J.

APPLICANT: Glucksmann, Maria A.

APPLICANT: Glucksmann, Maria A.

TITLE OF INVENTION: NOVEL THEKE, 9 alpha2delta-4, 54414, AND 53763 MOLECULES

TITLE OF INVENTION: AND USES THEREPOR

TITLE OF INVENTION WIMBER: US 60/185,938

PRIOR PILING DATE: 2000-02-29

PRIOR PILING DATE: 2000-02-29

PRIOR PELING DATE: 2000-02-29

PRIOR PILING DATE: 2000-03-03

PRIOR FILING DATE: 2000-03-03

PRIOR PILING DATE: 2000-03-03

PRIOR PILING DATE: 2000-04-07
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PRIOR FILING DATE: 2001-04-25
PRIOR PILING DATE: 2001-09-19
PRIOR PILING DATE: 2001-09-19
PRIOR PILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-09-35
PRIOR FILING DATE: 2001-09-35
SOFTWARE: PATENTING DATE: 2001-09-35
SOFTWARE: PATENTING DATE: 2001-09-37
NUMBER OF SEQ ID NOS: 85
SEQ ID NO 18
THENDER OF SEQ ID NOS: 85
SEQ ID NO 18
THENDER OF SEQ ID NOS: 85
                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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US-10-146-733-18
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Best Local Similarity
Matches 394; Conserv
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US-10-146-733-8
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AEVLHFQSMCSCLWYKSREKLQYSIPWIIPRDLSTSDTCVEQSHSSPGGGRYSDTPSRR 360
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PRIOR FILING DATE: 2000-04-11
PRIOR FILING DATE: 2000-04-26
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-19
PRIOR PELICATION NUMBER: US 60/235,018
PRIOR APPLICATION NUMBER: US 60/235,018
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-12-15
PRIOR PELICATION NUMBER: US 60/256,240
PRIOR FILING DATE: 2000-12-18
PRIOR PILING DATE: 2000-12-18
PRIOR PILING DATE: 2000-12-18
PRIOR PILING DATE: 2001-02-8
PRIOR FILING DATE: 2001-02-8
PRIOR FILING DATE: 2001-03-8
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2001-04-16
PRIOR FILING DATE: 2001-04-16
PRIOR FILING DATE: 2001-04-16
PRIOR FILING DATE: 2001-04-16
PRIOR FILING DATE: 2001-04-15
PRIOR FILING DATE: 2001-04-15
PRIOR FILING DATE: 2001-04-15
PRIOR FILING DATE: 2001-04-15
PRIOR FILING DATE: 2001-09-19
PRIOR FILING DATE: 2001-09-25
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PRIOR PRIOR
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US-10-146-733-8
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APPLICANT: Lease, Florian
APPLICANT: Fink, Michel
APPLICANT: Leasunski, Michel
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
FILE REFERENCE: 1201-CIP-DIV.00
CURRENT APPLICATION NUMBER: 05/049, 484
CURRENT FILING DATE: 2001-08-24
PRIOR FILING DATE: 1998-09-01
PRIOR PELING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 06/095, 234
PRIOR FILING DATE: 1998-09-04
PRIOR FILING DATE: 1998-09-04
PRIOR FILING DATE: 1998-09-04
PRIOR FILING DATE: 1998-09-04
PRIOR FILING DATE: 1998-03-04
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                                                                                                                                                                                                                                                                              241 LVVLRFWTWNAEDEKRDAEHRALLTRNGQAGGGG------GGSAHTTDTASSTAAA- 291
                                                                                                                                                                                                                                                                                                                      242 LVVLRFWTWNAEDEKRDAEHRALLTHNGQAGGLGGLSCLSGSLGDGVRPRDPVTCAAAAG 301
                                                                                                                                                                                                                                                                                                                                                                                                                         ------GGGGFRNVYABVLHFQSMCSCLWYKSREKLQYSIPMIIPRDLSTSDTCVEQS 343
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                                                                                                                                   181 YEHWTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQYVAFSFVYILTGLTVIGAFLN
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Pred. No. 6.8e-160;
9; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/09939484; Patent No. US20020032322A1; GENERAL INFORMATION: APPLICANT: Duprat, Fabrice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 88.1%;
Matches 357; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
US-09-939-484-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 405
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Pred. No. 8.3e-163;
8; Mismatches 23;
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Best Local Similarity 88.3%;
Matches 363; Conservative
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/ ORGANISM: Rattus norvegicus
US-10-146-733-9
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US-09-746-491-61
Sequence 61, Application US/09746491
Sequence 61, Application US/09746491
Sequence 61, Application US/09746491
Sequence 61, Application US/09746491
Sequence 61, Application US/090137202A1
Fater No. 1020020137202A1e1
FILE REFERENCE: 15966-621
CURRENT APPLICATION NUMBER: US/09/746,491
CURRENT FILING DATE: 2000-12-20
FRIOR APPLICATION NUMBER: USSN 60/171,329
FRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 BLERVVLRLKPHKAGVQWRPAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYALLGIPL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 TLVMFQSLGERINTLVRYLLHRAKKGLGMRRADVSMANNVLIGFFSCISTLCIGAAAFSH 180
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| Publication No. US20030165806A1
| GENERAL INFORMATION:
| APPLICANT: Price, Laura A. APPLICANT: Price, Laura A. APPLICANT: Price, Encaping H. TITLE OF INVENTION: Pocassium Channels, Nucleotide Sequences; TITLE OF INVENTION: Procassium Channels, Nucleotide Sequences; NUMBER OF SEQUENCES: 56
| CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1278; DB 9; Length 258;
Pred. No. 5.7e-110;
5; Mismatches 5; Indels
394
                                      405
350 GGRYSDTPSRRCLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV
                       361 GGRYSDTPSHPCLCSGTQRSAISSVSTGLHSLAAFRGLMKRRSSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: American Home Products Corporation STREET: One Campus Drive CITY: Parsippany STATE: New Jersey COUNTRY: USA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVVLRFMTMNAEDEKRDA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62.6%;
96.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 248; Conservative
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; ORGANISM: Mus musculus
US-09-746-491-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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US-08-816-011-55
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                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 258
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GENERAL INFORMATION:

APPLICANT: Duprat, Fabrice

APPLICANT: Leadunski, Michel

APPLICANT: Leadunski, Michel

APPLICANT: Lazdunski, Michel

TITLE OF INVENTION: UNMER: 105/09/939,483

CURRENT FILING DATE: 1998-09-01

PRIOR APPLICATION NUMBER: 09/14,914

PRIOR APPLICATION NUMBER: 60/055,234

PRIOR APPLICATION NUMBER: FR 96/01565

PRIOR APPLICATION NUMBER: FR 96/01565

PRIOR APPLICATION NUMBER: FR 96/01565

WUMBER OF SEQ ID NOS: 24

SOFUND NO SEC 10 NOS: 24

SEQ ID NO S.

LENGTH: ABL
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                             301 GVGGSGFRNVYAEVLHFQSMCSCLWYKSREKLQYSIPMIIPRDLSTSDTCVEHSHSSPGG 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               292 --GGGGFRNVYAEVLHFQSMCSCLWYKSREKLQYSIPMIIPRDLSTSDTCVEQSHSSPGG 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GVGGSGFRNVYAEVLHFQSMCSCLWYKSREKLQYSIPMIIPRDLSTSDTCVEHSHSSFGG 360
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                                                                                   ---GGGGFRNVYAEVLHFQSMCSCLWYKSREKLQYSIPMIIPRDLSTSDTCVEQSHSSPGG
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                                                                                                                                                                                         GGRYSDTPSHPCLCSGTQRSAISSVSTGLHSLAAFRGLMKRRSSV 405
                                                                                                                                                               GGRYSDIPSRRCLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394
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llarity 88.1%; Pred. No. 6.8e-160;
Conservative 9; Mismatches 25;
                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/09939483 Patent No. US20020094558A1
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US-09-939-483-5
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Best Local Similarity
Matches 357; Conserv
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ORGANISM: Murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 405
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59.9%;
83.1%;
                                         Query Match 59.9
Best Local Similarity 83.1
Matches 250; Conservative
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 233
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         US-10-870-492-55
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Sequence 55, Application US/10870492

Publication No. US20050032165A1

SERBEAL INFORMATION:

APPLICANT: PADSCH, MARK H.

TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,

TITLE OF INVENTION: ADM METHODS OF USING SAME

FILE REPERENCE: 01142.0114 SEQUENCE LISTING

CURRENT FILING DATE: 2004-06-18

FRIOR APPLICATION NUMBER: US/10/870,492

PRIOR FILING DATE: 2000-02-15

PRIOR FILING DATE: 1997-03-11

PRIOR FILING DATE: 1995-10-25

PRIOR APPLICATION NUMBER: 07/332,312

PRIOR APPLICATION NUMBER: 07/332,312

PRIOR FILING DATE: 1994-10-31

NUMBER OF SEQ ID NOS: 74

SEQ ID NO 55

LENGTH: 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 RVVLRLKPHKAGVQWRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYALLGIPL 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 TLVMFQSLGERINTLVRYLLHRAKKGLGMRRADVSMANMVLIGFFSCISTLCIGAAAFSH 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LNLVVLRFMTMNAEDEKRDAEHRALLTRNGQAGGGG-----GGSAHTTDTASSTAA 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        250 INLVVLREMTMNAEDEKRDAEHRALLTHNGQAVGLGGLSCLSGSLGDGVRPRDPVTCAAA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RVVLRLKPHKAGVQWRFAGSFYFAITVITTIGYGHAAPSTDGGKV---FCMFYALLGIPL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    133 TLVMFQSLGERINTSVRYLLHRAKRGLGMRHAEVSMANMVLIGFVSCISTLCIGAAAFSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 YEHWIFFQAYYYCFITLTIGFGDYVALQXDQALQTQPQYVAFSFVYILTGLTVIG--AF
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                                                                                                                                                                                                                                                                                                                                                                                             16;
                                                                                                                                                                                                                                                                                                                                                     59.9%; Score 1224; DB 8; Length 312;
83.1%; Pred. No. 7.4e-105;
tive 8; Mismatches 27; Indels 1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,011
FILING DATE: 11-MAR-1997
CLASSIFFCATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Matthews, Gale F.
REGISTRATION NUMBER: 32,269
REFERENCE/DOCKET NUMBER: 32,421-C2
TELECHANNICATION INFORMATION:
TELEPHONE: 201-683-2134
TELEPHONE: 201-683-2134
TELEPHONE: 201-683-8117
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 312 amino acids
TYPE: amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 83.1
Matches 250; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    310 Å 310
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US-08-816-011-55
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| VS-10-459-190-15
| Sequence 15, Application US/10459190
| Publicatation No. US20040072216A1
| Sequence 15, Application US/040072216A1
| GENERAL INFORMATION:
| APPLICANT: Palma, John F.
| APPLICANT: Schweitzer, Anthony C.
| APPLICANT: Blume, John F.
| APPLICANT: Metabolex, Inc.
| APPLICANT: Metabolex, Inc.
| TITLE OF INVENTION: Diabetes
| TITLE OF INVENTION: Diabetes
| FILE REFERENCE: 016325-008210US
| CURRENT APPLICATION NUMBER: US/10/459,190
| CURRENT FILING DATE: 2003-06-10
| PRIOR APPLICATION NUMBER: US 60/387,642
| PRIOR APPLICATION NUMBER: US 002-06-10
                                                                                                                                                                                                                                                                                     64 RVVLRLKPHKAGVQWRFAGSFYFAITVITTIGYGHAAPSTDGGKV---FCMFYALLGIPL 120
                                                                                                                                                                                                                                                                                                                                      73 RVVLRIKPHKAGVQWRPAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFCMFYALLGIPL 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             250 INLVVIREMTWINEDEKRDAEHRALLTHINGQAVGLGGLSCLSGSLGDGVRPRDPVTCAAA 309
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                                                                                                                                         4 QNVRTLALIVCTFTYLLVGAAVFDALESEPELIERQRLELRQQELRARYNLSQGGYEELE 63
                                                                                                                                                                                 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    193 YERWIFFQAYYYCFIILITIGFGDYVALQKDQALQTQPQYVASA---SCTSSRAHGHRRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RILALIVCTFTYLLVGAAVFDALESEPEMIERQRLELRQLELRARYNLSEGGYEELERVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239 LNLVVLRFWTWNAEDEKRDAEHRALLTRNGQAGGGG------GGSAHTTDTASSTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 YEHWTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQYVAFSFVYILTGLTVIG--AF
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                                                                      16;
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Length 312;
                                                                  Indels
Score 1224; DB 17;
Pred. No. 7.4e-105;
8; Mismatches 27;
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us-09-503-089a-5.rapb

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TITLE OF INVENTION: HOWDEL TWIK-6, TWIK-7, IC:
TITLE OF INVENTION: HNMDA-1, TWIK-9, alpha27
TITLE OF INVENTION: AND USES THEREPOR
FILE REFERENCE: MN1-248
CURRENT FILING DATE: 2002-05-15
PRIOR PEDLICATION NUMBER: US (0/18; 938
PRIOR PELLING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: US (0/18; 938
PRIOR PLLING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US (0/19; 734
PRIOR PLLING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: US (0/19; 734
PRIOR PLLING DATE: 2000-04-07
PRIOR PLLING DATE: 2000-04-07
PRIOR PLLING DATE: 2000-04-19
PRIOR PLLING DATE: 2000-04-16
PRIOR PLLING DATE: 2000-04-16
PRIOR PLLING DATE: 2000-09-19
PRIOR PLLING DATE: 2000-12-18
PRIOR PLLING DATE: 2000-12-28
PRIOR PLLING DATE: 2001-02-28
PRIOR PLLING DATE: 2001-02-28
PRIOR PLLING DATE: 2001-04-19
PRIOR PLLING DATE: 2001-04-25
PRIOR PLLING DATE: 2001-04-25
PRIOR PLLING DATE: 2001-04-25
PRIOR PLLING DATE: 2001-04-25
PRIOR PPLICATION NUMBER: US 09/964, 255
PRIOR PPLING DATE: 2001-09-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 59.0%
Matches 233; Conservative
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                                                                                                                                                                                                                                                                                                    APPLICANT: Wo. David
APPLICANT: Powers, Scott
APPLICANT: Powers, Scott
APPLICANT: Powers, Scott
APPLICANT: Powers, Scott
APPLICANT: Tularik Inc.
TITLE OF INVENTION: KCNB: A No. US20020102676Alel Potassium Channel Protein
FILE REFERENCE: 018791-004010US
CURRENT APPLICATION NUMBER: US/09/798,584
CURRENT FILING DATE: 2001-03-03
PRIOR APPLICATION NUMBER: US 60/186,951
PRIOR APPLICATION NUMBER: US 60/186,951
NUMBER OF SEQ ID NOS: 18
SCFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 TLVMPQSLGERINTLVRYLLHRAKKGLGMRRADVSMANMVLIGFFSCISTLCIGAAAFSH 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 LVVLRFMTMNAEDEKRDAEHRALLTRNGQAGGGGGGGSAHTTDTASSTAAAGGGGGFRNVY 300
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          1 MKRQNVRTLALIVCTFTYLLVGAAVFDALESEPELIERQRLELRQQELRARYNLSQGGYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 LVVLRFLTMNSEDERRDAEERASL-----AGNRNSMVIHIPEEPRPS------RPRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 YEHWIFFQAYYYCFITLITIGFGDYVALQKDQALQTQPQYVAFSFVYILTGLTVIGAFLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: human KCNB (Potassium Channel expressed in Breast)
US-09-798-584-1
                                                                                                                  181 FQAYYYCFITLTTIGFGDYVALQKDQALQTQFQYVAFSFVYILTGLTVIGAFL 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22;
                                                                                         FOAYYYCFITLTTIGFGDYVALQKDQALQTQPQYVAFSFVYILTGLTVIGAFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.7%; Score 1116; DB 9; Length 3
59.0%; Pred. No. 9.7e-95;
tive 44; Mismatches 96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360 RCLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394
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Publication No. US20030165891A1
GENERAL INFORMATION:
APPLICANT: Curtis, Rory A.J.
APPLICANT: Glucksmann, Maria A.
APPLICANT: Silos-Santiago, Inmaculada
                                                                                                                                                                                                                                                           Sequence 1, Application US/09798584 Patent No. US20020102676A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 59.09
Matches 233; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
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K-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615, TWIK-9, alpha2delta-4, 54414, AND 53763 MOLECULES
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59.0%; Pred. No. 9.7e-95;
iive 44; Mismatches 96; Indels 22
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Qy 301 -AEVLHPOSMCSCLWYKSREKLQYSIPMIIPRDLSTSDTCVEQSHSSPGGGGRYSDTPSR 359 L

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Sequence 14, Appl
Sequence 8, Appli
Sequence 2, Appli
Sequence 83, Appl
Sequence 7001, Ap
Sequence 7368, Ap
Sequence 2, Appli
Sequence 6913, Ap
Sequence 7809, Ap
Sequence 7809, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
                                                                             July 13, 2005, 08:10:49; Search time 25.273 Seconds (without alignments) 1163.760 Million cell updates/sec
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(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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(cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-236-080-2

US-09-236-080-2

US-09-343-016-7368

US-09-949-016-7368

US-09-949-016-7368

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US-09-432-470-2

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US-09-362-842-69
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Maximum Match 100%
Listing first 45 summaries
                                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Sequence 4, Application US/09144914

Sequence 4, Application US/09144914

Patent No. 6309855

GENERAL INFORMATION:
APPLICANT: Duprat, Fabrice
APPLICANT: Lesage, Florian
APPLICANT: Lesage, Florian
APPLICANT: Estadunski, Michel
APPLICANT: Estadunski, Michel
APPLICANT: Fink, Michel
APPLICANT: Lesage, Florian
APPLICANT: By Michel
APPLICANT: By Michel
APPLICANT: By Michel
APPLICANT: By Michel
APPLICANT: By NOWINGER: US/09/144,914
CURRENT APPLICATION NUMBER: US/09/144,914
CURRENT APPLICATION NUMBER: 06/095,234
EARLIER PILING DATE: 1998-08-04
BARLIER APPLICATION NUMBER: FR 96/01565
BARLIER APPLICATION NUMBER: FR 96/01565
SAFLIER APPLICATION NUMBER: FR 96/01565
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIN Ver. 2.0
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                             11, Appl
11, Appli
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US-08-332-312-4

US-09-561-763-11

US-09-362-842-6

US-08-332-312-2

US-09-949-016-6654

US-09-949-016-7794

US-09-362-842-67

US-09-362-842-67

US-09-362-842-67

US-09-362-842-67

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US-09-362-842-81

US-09-362-842-81

US-09-362-842-81

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US-09-362-842-10
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Best Local Similarity 100.
Matches 394; Conservative
  336
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ORGANISM: Homo sapiens
    SEQ ID NO 4
LENGTH: 394
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US-09-144-914-4
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2, Appli 69, Appl 31685, A 81, Appl

Sequence Seq

Sequence Sequence

Sequence

1-09-431-367B-8 3-09-561-763-5 3-09-431-367B-5 US-09-362-842-2

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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                               ; OKGANISM: numal
US-09-949-016-7631
                                         RESULT 3
US-09-949-016-7631
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APPLICANT: Duprat, Fabrice
APPLICANT: Duprat, Fabrice
APPLICANT: Lesage, Florian
APPLICANT: Lesage, Florian
APPLICANT: Lazdunski, Michel
APPLICANT: Lazdunski, Michel
APPLICANT: Lazdunski, Michel
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
FILER REFERENCE: 989.6705CIP
CURRENT FILING DATE: 1996-01
EARLIER APPLICATION NUMBER: 08/79,816
EARLIER PILING DATE: 1996-11-15
EARLIER APPLICATION NUMBER: R 96/01565
EARLIER FILING DATE: 1996-02-08
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver: 2.0
SSEQ ID NO 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 292 --GGGGFRNVYAEVLHPQSMCSCLWYKSREKLQYSIPMIIPRDLSTSDTCVEQSHSSPGG 349
301 GVGGSGFRNVYAEVLHPQSMCSCLWYKSREKLQYSIPMIIPRDLSTSDTCVEHSHSSPGG 360
                                                                       AEVLHFQSMCSCLWYKSREKLQYSIPMIIPRDLSTSDTCVEQSHSSPGGGGRYSDTPSRR 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RVVLRLKPHKAGVQWRFAGSFYFALTVITTIGYGHAAPSTDGGKVFCMFYALLGIPLTLV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 MFQSLGERINTLVRYLLHRAKKGLGMRRADVSMANMVLIGFFSCISTLCIGAAAFSHYEH 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                        AEVLHFQSMCSCLWYKSREKLQYSIPMIIPRDLSTSDTCVEQSHSSPGGGGRYSDTPSRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 QNVRTLALIVCTFTYLLVGAAVFDALESEPELIERQRLELRQQELRARYNLSQGGYEELE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 89.1%; Score 1819; DB 3; Length 40 Best Local Similarity 88.1%; Pred. No. 3.6e-192; Matches 357; Conservative 9; Mismatches 25; Indels
                                                                                                               CLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394
                                                                                                                                 361 CLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394
                                                                                                                                                                                                           Sequence 5, Application US/09144914
Patent No. 6309855
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US-09-144-914-5
                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Murine
                          241
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Sequence 7631, Application US/09949016

Patent No. 6812339
GENERAL INPORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TURRENT PILING DATE: 2000-04-14
PRIOR REPEING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-00-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 200-012
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 7631
SEQ ID NO 7631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 195 CEEWSFFHAYYYCFITLTTIGFGDYVALQTKGALQKKPLYVAFSFMYILVGLTVIGAFLN 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 -AEVLHFOSMCSCLWYKSREKLOYSIPMIIPRDLSTSDTCVEOSHSSPGGGGRYSDTPSR 359
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Sequence 12, Application US/09362842

Patent No. 6511824

Patent No. 6511824

GENERAL INFORMATION:

APPLICANT: Buchman et al.

TITLE OF INVENTION: NUCLEIC ACIDS AND POLYPEPTIDES OF INVERTEBRATE TWIK

TITLE OF INVENTION: CHANNELS AND METHODS OF USE

FILE REFERENCE: 7326-104

CURRENT APPLICATION NUMBER: US/09/362,842

CURRENT PILING DATE: 1999-07-28

FRIOR APPLICATION NUMBER: 09/270,767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKRONVRTLALIVCTFTYLLVGAAVFDALESEPELIERORLELROGELRARYNLSOGGYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 MKRQNVRTLSLIVCTFTYLLVGAAVFDALESDHEMREBEKLKAEBIRIKGKYNISSEDYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVVLRFMTMNAEDEKRDAEHRALLTRNGQAGGGGGGGAHTTDTASSTAAAGGGGFRNVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22;
361 GGRYSDTPSHPCLCSGTQRSAISSVSTGLHSLAAFRGLMKRRSSV 405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 1116; DB 4;
; Pred. No. 1.7e-114;
44; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           358 NSLFP----SPISSISPGLHSFTDHORLMKRRKSV 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360 RCLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394
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59.0%;
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Best Local Similarity 59.0%
Matches 233; Conservative
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APPLICANT: Duprat, Fabrice
APPLICANT: Leasge, Florian
APPLICANT: Lazdunski, Michel
APPLICANT: Lazdunski, Michel
TITLE OF INVENTION: FAMILY OF MAMWALIAN POTASSIUM CHANNELS, THEIR CLONING
TITLE OF INVENTION: PAMILY OF MAMWALIAN POTASSIUM CHANNELS, THEIR CLONING
TITLE OF INVENTION: PAMILY OF MAMWALIAN POTASSIUM CHANNELS, THEIR CLONING
CURRENT APPLICATION NUMBER: US/09/144,914
CURRENT FILING DATE: 1996-11-15
EARLIER APPLICATION NUMBER: 06/095,234
EARLIER APPLICATION NUMBER: FR 96/01565
EARLIER PILING DATE: 1996-00-04
EARLIER PILING DATE: 1996-02-08
HUNDER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                       217 VFF-----LLLPAAIFASLEPEWDYLDSLYYCFISLTTIGLGDYI--PGDSAHQPYRPLY 269
                                                                                                                                                                                                                                                                                       270 KIMTTCYLFLGITIM--MLTLTVFYDIPQLNLGLLFTTSEDSEK------VRLASSGP 319
                                                                                     |||||::|||||||::|||||| CMFYAVVGIPLTLVVLLSALVERLLIPTVWLLQWLNSKLGHLYQPLRIRIVHLAIIVLVLL 216
                                                                                                                                                            163 GFFSCISTLCIGAAAFSHYE-HWTFFQAYYYCFITLTTIGFGDYVALQKDQALQT-QPQY 220
                                                                                                                                                                                                                                                      221 VAFSFVYILTGLTVIGAFLNLVV-----LRFWTWNAEDEKRDAEHRALLTRNGQAGG 272
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                                                              CMFYALLGIPLTLVMFQSLGERINTLVRYLLHRAKKGLG------MRRADVSMANMVLI 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKRQNVRTLALIVCTFTYLLVGAAVFDALESEPELIERQRLELRQQELRARYNLSQGGYE 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 18.1%; Score 370; DB 3; Length 370; Local Similarity 31.6%; Pred. No. 4.7e-32; nes 93; Conservative 57; Mismatches 102; Indels '
                                                                                                                                                                                                                                                                                                                                                        G---GGGGSAHTTDTASSTAAAGGGGFRNVYAEVLHFQS 308
                                                                                                                                                                                                                                                                                                                                                                                                   ----- NIHROVVRVRS 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/09144914
Patent No. 6309855
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                      320 GLOYGAGFSPHNED-
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ORGANISM: Murine
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELERVVLRLKPHKAGVQWRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYALLGIPL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 TLVMFQSLGERINTLVRYLLHRAKKGLGMRRADVSMANMVLIGFFSCISTLCI--GAAAF 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SHYEHWIFFQAYYYCFIILITIGFGDYVALQKDQALQTQPQYVAFSFVYILTGLTVIGAF 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------NISSMCSCHCICLNGNRHKKSSNLEKNNDAENQYKLRQSPT 338
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                                                                                                                                                                                                                                                                                                                                                           1 MKKQNVRTISLIVCTFTYLLVGAAVFDALESETEKRRWEALQDAEDMIIKKYNISQEDFK 60
                                                                                                                                                                                                                                                                                                                               1 MKRQNVRTLALIVCTFTYLLVGAAVFDALESEPELIERQRLELRQQELRARYNLSQGGYE 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLYPEPTIDES OF INVERTEBRATE TWIK
                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                             37.9%; Score 773; DB 4; Length 408; 43.6%; Pred. No. 1.5e-76; Live 66; Mismatches 82; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.6%; Score 379; DB 4; Length 361; 32.4%; Pred. No. 4.6e-33;
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Patent No. 6511824
GENERAL INFORMATION:
APPLICANT: Buchman et al.
TITLE OF INVENTION: CHANNELS AND METHODS OF USE
TITLE OF INVENTION: CHANNELS AND METHODS OF USE
CURRENT APPLICATION WUMBER: 1999-07-28
CURRENT FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: 09/270,767
PRIOR FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PATENTIN VET. 2.1
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                                                                                                                                                         ; ORGANISM: Drosophila melanogaster
US-09-362-842-12
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PRIOR FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
                                                                                                                                                                                                                             Query Match
Best Local Similarity 43.64
Matches 164; Conservative
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Best Local Similarity
Matches 110; Conserv
                                                                                                              LENGTH: 408
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FCMFYALLGIPLTLVMFQSLGERINTLVRYLLHRAKKGLGMRRAD------VSM 156
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98 ELDELIQQIVAAINAGIIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKI 157
                                                              FCMFYALLGIPLTLVMFQSLGERINTLVRYLLHRAKKGLGMRRAD-------VSM 156
                                                                                                 158 PCIIYALLGIPLFGFLLAGVGDQLGTIF-----GKGIAKVEDTFIKWNVSQTKIRI 208
                                                                                                                                            157 ANMVLIGFFSCISTLCIGAAAFSHYEHWTFFQAYYYCFITLTTIGFGDYVALQKDQALQT 216
                                                                                                                                                                   1 MKRONVRTLALIVCTFTYLLVGAAVFDALESEPELIERQRLELRQGELRARYNLSQGGYE 60
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31.0%; Pred. No. 3.3e-31;
ttive 59; Mismatches 102; Indels
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APPLICANT: Miller, Andrew P.
APPLICANT: Curran, Mark Edward
APPLICANT: Hu, Ping
APPLICANT: Rutter, Marc
APPLICANT: Wang, Jian Wang
TITLE OF INVENTION: No. 6399761el Human Potassium Channels
FILE REFERENCE: SEQ-15P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/336,643A CURRENT FILING DATE: 1999-06-18 PRIOR APPLICATION NUMBER: 60/076,687 PRIOR FILING DATE: 1998-08-07 PRIOR PRICATION NUMBER: 60/116,448 PRIOR FILING DATE: 1999-01-19 PRIOR PELICATION NUMBER: PCT/US99/03826 PRIOR PELING DATE: 1999-02-22
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 83
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; Sequence 83, Application US/09336643A
; Patent No. 6399761
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Best Local Similarity
Matches 91; Conserv
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US-09-949-016-7001
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17.8%; Score 363; DB 3; Length 411;
Best Local Similarity 31.0%; Pred. No. 3.3e-31;
Matches 91; Conservative 59; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Length 411;
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                                                         Sequence 6, Application US/09236080

Patent No. 6242217

GENERAL INFORMATION:
APPLICANT: Helen Meadows
TITLE OF INVENTION: No. 6242217e1 Compounds
FILE REFERENCE: GP30031
CURRENT FILING DATE: 1999-01-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
SSEQ ID NO 6
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APPLICANT: Helen Meadows
APPLICANT: Helen Meadows
ITILE OF INVENTION: No. 6242217el Compounds
FILE REFERENCE: GP30031
CURRENT APPLICATION NUMBER: US/09/236,080
CURRENT FILING DATE: 1999-01-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Mus musculus
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                                                   US-09-236-080-6
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124 ALVGIPLFGILLAGVGDRLGSSLRH-----GIGHIEAIFLKWHVPPELVRVLSAMLFL 176
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                                                                                                                                                    57 ---GGYEELERVVLRLKPHKAGVQWRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFY
                                                                                                           1 MKRQNVRTLALIVCTFTYLLVGAAVFDALESEPELIERQRLELRQQE-LRARYNLSQGGY
                                                  Gaps
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                                                  33;
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                                                  109; Indels
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                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/422,470 CURRENT FILING DATE: 1999-11-03 EARLIER APPLICATION NUMBER: UK 9923668.9 EARLIER FILING DATE: 1999-10-07 EARLIER APPLICATION NUMBER: UK 9824048.4 EARLIER FILING DATE: 1998-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 4 SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Conrad Gerald Chapman
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 2, Application US/09432470; Patent No. 6426197; GENERAL INFORMATION:
                                                  53;
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                                                     95; Conservative
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; ORGANISM: HOMO SAPIENS
US-09-432-470-2
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LENGTH: 393
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERRNET CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR PELING DATE: 2000-04-14
PRIOR PELING DATE: 2000-10-20
PRIOR PELING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-06
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JUNEAU INFORMATION:

JULIE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001301

FILE REFERENCE: CL001-0-14

CURRENT FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PLING DATE: 2000-10-0-3

PRIOR FILING DATE: 2000-10-0-3

PRIOR PELING DATE: 2000-10-0-3

PRIOR FILING DATE: 2000-0-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 7368

LENGTH: 558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 QELETLIQHALDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGK 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 VFCMFYALLGIPLTLVMFQSLGERINTLVRYLLHRAKKGLGMRRADVSMANM-----VLI 162
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32.8%; Pred. No. 1.5e-29;
tive 53; Mismatches 109
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US-09-949-016-7368
; Sequence 7368, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
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Best Local Similarity
Matches 95; Conserv
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Best Local Similarity
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US-09-949-016-7001
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SEQ ID NO 6913
LENGTH: 419
TYPE: PRT
ORGANISM: Human
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Patent No. 6812339

GENBRAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFREENCE: CLOA01307

CURRENT APPLICATION NUMBER: 06/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PELING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASELSEQ for Windows Version 4.0
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124 ALVGIPLFGILLAGVGDRLGSSLRH-----GIGHIEAIFLKWHVPPELVRVLSAMLFL 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57 ---GGYEELERVVLRLKPHKAGVQWRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
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16.1%; Score 329.5; DB 4;
Best Local Similarity 31.0%; Pred. No. 1.5e-27;
Matches 98; Conservative 43; Mismatches 112;
                                                                                                                            APPLICANT: David Malcolm Duckworth
APPLICANT: Conrad Gerald Chapman
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30190
CURRENT APPLICATION NUMBER: US/09/432,470
CURRENT FILING DATE: 1999-11-03
EARLIER FILING DATE: 1999-10-07
EARLIER FILING DATE: 1999-10-07
EARLIER FILING DATE: 1999-10-07
EARLIER FILING DATE: 1999-10-07
SARLIER FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 393
TYPE: PRT
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                                                                        Sequence 4, Application US/09432470 Patent No. 6426197 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  277 GSAHTTDTASSTAAAG 292
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US-09-949-016-6913
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| Facella No. colleged al. No. Craig et al. |
| GENERAL INFORMATION: |
| APPLICANT: VENTER, J. Craig et al. |
| APPLICANT: VENTER, J. Craig et al. |
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF; |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF; |
| CURRENT APPLICATION NUMBER: 60/241,755 |
| PRIOR FILING DATE: 2000-10-03 |
| PRIOR PLILING DATE: 2000-10-04 |
| PRIOR PLILING DATE: 2000-10-08 |
| PRIOR PLILING DATE: 2000-10-09 |
| PRIOR PLILING
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                                                                                         Length 419;
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                                                                                                                                                                                                                                                                               9 LALIVCTFTYLLVGAAVFDALESEPE-LIERORLELROQELRARYNLSO-
                                                                                                                                                                             Indels
                                                                               Query Match 16.1%; Score 329.5; DB 4; Best Local Similarity 31.0%; Pred. No. 1.7e-27; Matches 98; Conservative 43; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4;
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; Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       277 GSAHTTDTASSTAAAG 292
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; ORGANISM: Human
US-09-949-016-7809
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US-09-949-016-7809
US-09-949-016-6913
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July 13, 2005, 07:58:54; Search time 101.398 Seconds (without alignments) 1567.669 Million cell updates/sec Run on:

US-09-503-089A-4 2090 Title: Perfect score:

1 MAAPDLLDPKSAAQNSKPRL.....LNGLTPHCAGEDIAVIENMK 411 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2105692 seqs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04:* Database

geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp1980s:* geneseqp1990s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aael0342 Murine TR	Aay28497 Mouse h-T	Aay34133 Human pot		Aab50044 Human TRE	Adp03586 Human GPC	Adq76698 Human two	Aael0341 Human TRE	Adp03575 Human GPC	Aae16597 Human TWI	Aau07618 Human pot	Aau07622 Human pot	Aau07623 Human pot	Aau07625 Human pot	Aau07624 Human pot	Aay30648 A mechani	Abr41487 Human DIT	Aab47930 Human TRE	Aae16596 Human TWI	Abp69333 Human pol		Aau81354 Novel hum	Aau79472 Human nov	Abb83542 Hypothala	Ada05746 Human NOV
ΩI	AAE10342	AAY28497	AAY34133	AAY28496	AAB50044	ADP03586	ADQ76698	AAE10341	ADP03575	AAE16597	AAU07618	AAU07622	AAU07623	AAU07625	AAU07624	AAY30648	ABR41487	AAB47930	AAE16596	ABP69333	AAE21804	AAU81354	AAU79472	ABB83542	ADA05746
% Query Match Length DB	411 3	411 2	411 2	411 2	411 4	411 7	411 8	411 3	422 7	411 5	426 4	426 4	426 4	426 4	426 4	370 2	337 6	538 5	538 5		543 .5	543 5	543 5	<u>-</u>	543 · 6
& Query Match I	100.0	99.7	97.8	97.8	97.8	97.8	97.8	7.76	97.5	97.3	96.2	96.0	96.0	95.8	95.8	89.2	77.5	59.9	59.9	59.9	59.9	59.9	59.9	59.9	59.9
Score	2090	2084	2044	2044	2044	2044	2044	2041	2038	2033	2011	2007	2006	2003	2002	1864	1620.5	1251.5	1251.5	1251.5	1251.5	1251.5	1251.5	1251.5	1251.5
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ALIGNMENTS

Murine; potassium channel protein; TREK-1; anaesthetic; analgesia; Murine TREK-1 potassium channel protein. AAE10342 standard; protein; 411 AA 11-FEB-2000; 2000WO-IB000226. 12-FEB-1999; 99US-0119727P. 11-FEB-2000; 2000US-00503089. ·10-DEC-2001 (first entry) WO200047738-A2. Mus musculus. 17-AUG-2000. AAE10342; amnesia. RESULT 1

(CNRS) CNRS CENT NAT RECH SCI

Patel AJ; Lesage F, Romey G, ω, Lazdunski M, Honore

WPI; 2000-549146/50. N-PSDB; AAD17497. Novel nucleic acid encoding a TREK-1 potassium channel protein for transfecting cells to be used to identify compounds with anesthetic properties.

Claim 9; Page 32-33; 39pp; English.

The invention relates to human and mouse TREK-1 potassium channel proteins and their corresponding DNA molecules. TREK-1 nucleic acid is useful for transfecting cells to induce expression of the TREK-1 potassium channel protein. These cells are then used in assays to identify compounds which have anaesthetic properties, producing a safe, reversible state of unconsciousness with concurrent amnesia and analgesia in a mammal upon inhalation. The present sequence is murine TREK-1 potassium channel protein

Sequence 411 AA;

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N-PSDB; AAZ11915.
                                                                        Local Similarity
                                                 Sequence 411 AA;
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                                                                                                  SNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180
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                                          MAAPDILDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKWTVSTIFLVVVLYLI
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; Score 2090; DB 3;
; Pred. No. 3.5e-218;
0; Mismatches 0;
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tch 100.0%; al Similarity 100.0%; 411; Conservative 0
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chromosome 1q32
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polypeptides. The methods of diagnosis may be used in the treatment of diseases including cancer, pulmonary, cardiovascular, and inflammatory diseases, pain, psychiatric disorders including depression and schizophrenia, neurodegenerative diseases including Alzheimer's, stroke, and head trauma and neurological disorders including migraine
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99.8%; Pred. No. 1.6e-217;
iive 0; Mismatches 1;
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(first entry)

12-OCT-1999

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controlled the representation of the control of the
New nucleic acids encoding mammalian K+Hnov potassium channel proteins, useful-for the diagnosis and treatment of episodic ataxia with myokymia cardiac arrhythmia, epilepsy and Bartter's syndrome.
                                                                                                                                                                                                                                    sequence represents the human K+Hnov59 potassium channel. K+Hnov
                                                                                                                                                         Claim 3; Page 104-105; 112pp; English
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ö 120 180 240 240 GAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS 120 SNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180 AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS 300 300 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSAELAGNHNQ 360 9 SNOVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ LGTIFGKGIAKVEDTFIKMNVSQTKIRIISTIIFILFGCVLFVALPAVIFKHIEGWSALD LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAIFKHIEGWSALD AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS 1 MAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVVLYLII Gaps 1 MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVVLYLII ELTPCRRTLSVNHLTSEREVLPPLLKAESIYLNGLTPHCAGEDIAVIENMK 411 .. 0 Length 411; Indels Query Match 97.8%; Score 2044; DB 2; Best Local Similarity 96.4%; Pred. No. 3.5e-213; Matches 396; Conservative 11; Mismatches 4; •• Sequence 411 AA; 301 181 301 361 61 121 121 61 g a 셤 ò 8 ઠ 셤 ઠે g ò 셤 ઠે ò

KKTKEEVGEFRAHAAEWTANVTAEFKETRRLSVEIYDKFQRATSVKRKLSAELAGNHNQ 360 AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS ELTPCRRTLSVNHLTSEREVLPPLLKAESIYLNGLTPHCAGEDIAVIENMK 411 241 301 241 301 361 δ 셤 ð 음 AAY28496 standard; protein; 411 AA 361

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polynucleotide AAZ0003, h-TREKI is a two pore potessium channel, and the gene maps to human chromosome 1q32, between the markers D1S237 and wis 15105. The polynucleotide sequence of h-TREKI can be used to diagnose a disease or susceptibility to a disease related to expression or activity of h-TREK-1 polypeptides. The methods of diagnosis may be used in the treatment of diseases including cancer, pulmonary, cardiovascular, and inflammatory diseases, pain, psychiatric disorders including depression and schizophrenia, neurodegenerative diseases including Alzheimer's, stroke, and head trauma and neurological disorders including migraine.
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                                                        h-TREK1; two pore potassium channel; inflammatory disease; chromosome 1q32.
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Matches 396; Conservative
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N-PSDB; AAZ00039.
                            h-TREK1 polypeptide
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                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modulators of h-TREK1 polypeptides for treating epilepsy, sleep-related disorders, addiction and dyskinesias including Parkinson's and
                                                                                                                                                                                                                          Human; TREK; 2P domain potassium channel; resting membrane potential; neuronal excitability; neurotransmitter release modulation; epilepsy; neurological disorder; sleep-related disorder; cognitive dysfunction; attention deficit disorder; addiction; anxiety; phobia; Parkinson's chorea; Huntington's chorea; cerebral palsy; incontinence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GATVEKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQIVAAINAGIIPLGNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human TREX1 polypeptide, polynucleotides encoding them and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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361 ELTPCRRTLSVNHLTSERDVLPPLLKTESIYLNGLTPHCAGEEIAVIENIK
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96.4%; Pred. No. 3.5e-213;
ive 11; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Randall AD;
                                                                                       Ą
                                                                                       AAB50044 standard; protein; 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 7; Page 29; 35pp; English.
                                                                                                                                                                                                                                                                                                                  erectile dysfunction; alopecia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SMIK ) SMITHKLINE BEECHAM PLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99GB-00012733.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2000; 2000WO-GB002107.
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Best Local Similarity 96.4%
Matches 396; Conservative
                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Meadows HJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Huntington's chorea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI: 2001-080422/09.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                         19-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                    07-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hervieu GJ,
                                                                                                                                                                                           Human TREK
                                                                                                                       AAB50044;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPCR; G-protein coupled receptor; neuroprotective; nootropic; tranquiliser; antimigraine; neuroleptic; antimanic; antidepressant; anticonvulsant; antiparkinsonian; cytostatic; cardiant; hypotensive; antianginal; analgesic; anorectic; anti-HIV; antiasthmatic; osteopathic; uropathic; antiulcer; antiallergic; cell cycle regulation; neurological; severe mental retardation; dyskinesia; brain; spinal cord; affective; neoplastic; cardiovascular; immunological; immune; endocrinal; growth; chromosome identification; metabolic; pituitary; chromis endocrinal; potassium channel subfamily K member 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid molecule encoding a human G-protein coupled receptor, useful for diagnosing, preventing or treating diseases involving the receptor, e.g. Parkinson's disease, dementia, asthma, hypertension or
KKTKEEVGEFRAHAAEWTANVTAEFKETRRLSVEIYDKFORATSVKRKLSAELAGNHNO
                                                                                                                 241 AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS
                                                                                                                                                                                                                                                                                                                                                                                                                                           ELIPCRRILSVNHLISEREVLPPLLKAESIYLNGLIPHCAGEDIAVIENMK 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human GPCR potassium channel, subfamily K, member 2 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; SEQ ID NO 31; 224pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADP03586 standard; protein; 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-JAN-2003; 2003WO-US001911.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disorders, immune-related disorders, endocrinal diseases, growth disorders, eating disorders, HIV infection, cancers, metabolic disorders and pitulitary disorders. Furthermore, the polymucleotide may be used in chromosome identification, in identifying organisms from minute biological samples, in gene therapy or as a molecular weight marker. The current sequence is that of a human GPCR (G-protein coupled receptor) protein of the invention which was used for homology purposes.
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neoplastic disorders, cardiovascular disorders, immunological
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      two pore domain potassium channel; sedative; hypnotic;
                                                                                                                                                                                               Gaps
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                                                                                                                                                             Query Match 97.8%; Score 2044; DB 7; Best Local Similarity 96.4%; Pred. No. 3.5e-213; Matches 396; Conservative 11; Mismatches 4;
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GENBANK; NM014217.
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                                                                                                                                   Sequence 411 AA;
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                                                                                                                  The present sequence is that of the human two pore domain K+ channel TREK -1. In rate, TREK-1 is highly expressed in much of the brain and is inhibited by protein kinase C and protein kinase C mediated by protein kinase C mediated by by cortain and on experimental results, it is hypothesized that TREK-1 is activated by volatile general anaesthetics and is expressed at high levels in the brain of sleep animals. Based on these expressed at high levels in the brain of sleep animals. Based on these key mediator of sleep (when open) and waking (when closed). The invention provides methods for identifying a sleep- or wakefulness-promoting compound based on the compound's ability to modulate two pore domain K+ channels such as TREK-1. It also provides screening methods for isolating short sleep, no rebound and sleep deprivation resistant Drosophila mutants useful for identifying sleep-related molecular targets.
               Identifying a Drosophila mutant fly with a no rebound, short sleep and/or no sleep deprivation resistant phenotype, for identifying sleep-related molecular targets, comprises recording sleep quantity of the mutant fly.
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                                                                                                                                                                                                                                                                                                                                                                                                 Length 411;
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Pred. No. 3.5e-213;
                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Mismatches
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                                                                                      NO 2; 83pp; English
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Best Local Similarity
Matches 396; Conserv
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                                                                                      12; SEQ ID
                                                                                                                                                                                                                                                                                                                                                             Sequence 411 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                              Novel nucleic acid encoding a TREK-1 potassium channel protein for transfecting cells to be used to identify compounds with anesthetic
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                                                                                                 Patel AJ;
                                                                                                                                                                                                                                                                                                                                                                                                           4;
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; Pred. No. 7.5e-213;
12; Mismatches 4;
                                                                                                 Romey G,
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                                                                                                 Lesage F,
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                                                                                                                                                                                                                 Claim 3; Page 28; 39pp; English
                                                                        CENT NAT RECH SCI
                                                                                                                                                                                                                                                                                                                                                                                 97.7%;
96.1%;
           11-FEB-2000; 2000WO-IB000226.
                                               2000US-00503089.
                                     99US-0119727P
                                                                                                                                                                                                                                                                                                                                potassium channel protein
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Best Local Similarity 96.1<sup>†</sup>
Matches 395; Conservative
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                                                                                                 Honore
                                                                                                                           2000-549146/50.
                                                                                                                                       N-PSDB; AAD17496
                                                                                                                                                                                                                                                                                                                                                         Sequence 411 AA;
                                                                                                 Lazdunski M,
                                                  11-FEB-2000;
                                                                        (CNRS ) CNRS
                                     12-FEB-1999;
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Human GPCR twin pore channel" protein variant "Gene 9" protein.

(first entry)

29-JUL-2004

ADP03575

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The invention relates to a novel isolated GPCR (G-protein coupled receptor) nucleic acid molecule. The polynucleotide and polypeptide of the invention demonstrate neuroprotective, nootropic, tranquiliser, antimigraine, neuroleptic, antimanic, antidepressant, anticonvulsant, antiparkinsonian, cytostatic, antimatic, antidepressant, anticonvulsant, antiparkinsonian, cytostatic, antiasthmatic, osteopathic, uropathic, analgesic, anorectic, anti-HIV, antiasthmatic, osteopathic, uropathic, antiparkinsonian, properties. The nucleic acid molecule and polypeptide of the invention may be useful in diagnosing, preventing, treating or ameliorating a medical condition, such as a disorder related to aberrant coll cycle regulation, neurological disorders, severe mental retardation and dyskinesias, brain disorders, spinal cord disorders, immunological disorders, indisorders, immunological disorders, endocrinal diseases, growth disorders, eating disorders, HIV infection, cancers, metabolic disorders and pituitary disorders. Furthermore, the polynucleotide may be used in chological samples, in gene therapy or as a molecular weight marker. The current sequence is that of a human GPCR (G-protein coupled receptor) protein which was isolated by the method of the invention.
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GPCR; G-protein coupled receptor; neuroprotective; nootropic; tranquiliser; antimigraine; neuroleptic; antimanic; antidepressant; antideorial antiperkinsonian; cytostatic; cardiant; hypotensive; antianginal; antiparkinsonian; cytostatic; cardiant; hypotensive; antianginal; analgesic; ancectic; anti-HIV; antiasthmatic; osteopathic; uropathic; antiulcer; antiallergic; cell cycle regulation; neurological; severe mental retardation; dyskinesia; brain; spinal cord; affective; neoplastic; cardiovascular; immunological; immunne; endocrinal; growth; cating; HIV infection; cancer; metabolic; pituitary; chromosome identification; gene therapy; human; receptor; twin pore channel; potassium channel subfamily K member 2 variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid molecule encoding a human G-protein coupled receptor, useful for diagnosing, preventing or treating diseases involving the receptor, e.g. Parkinson's disease, dementia, asthma, hypertension or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVVLYLII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Feder JN;
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                                                                                                                                                                                                                                                                                                                                                   22-JAN-2003; 2003WO-US001911.
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N-PSDB; ADP03564.
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and moderately in testis, brain, colon and small intestine. The mammalian K+ channel protein is useful in methods for screening various compounds. In particular, the protein is useful in methods for identifying biologically active compounds with anaesthetic properties. The present sequence is TREK-1 protein used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane potassium ion channel protein; inward potassium flux; pest control; membrane potential; pesticide; antihelminthic; nematode;
                                                                                                                                                                                                                                                                                                  61 GATVFKALEQPHEISQRTTIVIQKQTPISQHSCVNSTELDELIQQIVAAINAGIIPLGNT
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                                                                                                                                        Length 411;
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                                                                                                                                        97.3%; Score 2033; DB 5; 95.9%; Pred. No. 5.6e-212;
                                                                                                                                                                          12; Mismatches
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                                                                                                                                                          Similarity
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                                                                                                       Sequence 411 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a mammalian K+ channel protein with two pore domains, called TREK2 (TWIK-Related K+ Channel). The protein produces currents whose current-voltage relationship is slightly inwardly rectifying in high symmetrical K+ conditions. TREK2 is a member of the fatty acid-activated and mechanosensitive K+ channel family. TREK-2 gene located on chromosome 14q31 is abundantly expressed in kidney, pancreas
                                         LGTIFGKGIAKVEDTFIKWANSQTKIRIISTIIFILFGCVLFVALPAIIFKHIEGWSALD
                                                                                       AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS
                                                                                                           AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS
                                                                                                                                                          KKTKEEVGEFRAHAAEWTANVTAEFKETRRLSVEIYDKFQRATSVKRKLSAELAGNHNQ
                                                                                                                                                                             KKTKEEVGEFKAHAAEWTANVTAEFKETRRRLSVEIYDKFORATSIKRKLSAELAGNHNO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New mammalian K+ channel protein with two pore domains, for screening various compounds, particularly for identifying biologically active compounds with anesthetic properties.
                                                                                                                                                                                                                                              TWIK-Related K+ Channel-1, TREK-1; anaesthetic; screening,
                                                                                                                                                                                                                              411
                                                                                                                                                                                                                              ELTPCRRTLSVNHLTSEREVLPPLLKAESIYLNGLTPHCAGEDIAVIENMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "P2 pore domain"
274. .293
/note= "M4 membrane spanning segment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     segment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 segment'
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human TWIK-Related K+ Channel-1 (TREK-1) protein
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127. 150
/note= "P1 pore domain"
158. 178
/note= "M2 membrane spanning se
209. 230
/note= "M3 membrane spanning se
236. 259
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                                                                                                                                                                                                                                                                                                                                                  AAE16597 standard; protein; 411
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2001US-00892360.
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27-JUN-2001;
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23-AUG-2001
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                                          The invention relates to a mutant potassium ion channel protein, having four membrane spanning domains and two pore forming domains, comprising a mutation at the second pore forming domain. The expression of the mutant protein in a cell confers improved inward potassium flux and the ability to grow in the presence of potassium. Mutant proteins and their corresponding polynucleotide sequences can therefore be used to improve the membrane potassium flux into cells under acidic conditions by modulating the membrane potential using therapeutic agents. The sequences may be used to develop agonists and annegonists of potassium channel proteins in order to control pests such as nematodes and insects. This sequence
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                                                                                                                                                                                                                                                                          75
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                                                                                                                                                                                                                                                                                                  GAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS
                                                                                                                                                                                                                                                                                                                                              SNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ
                                                                                                                                                            represents a human transmembrane potassium ion channel protein, TPKC1
                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                          Length 426;
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/note= "Wild-type Ala replaced by Thr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human potassium ion channel TPKC1 mutant protein #1
                                                                                                                                                                                                         96.2%; Score 2011; DB 4;
llarity 95.1%; Pred. No. 1.5e-209;
Conservative 13; Mismatches 7;
  inward potassium flux under acidic conditions.
                         Example 15; Page 45; 131pp; English
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                                                                                                                                                                                     Sequence 426 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a mutant potassium ion channel protein, having mutation at the second pore forming domains, comprising a mutation at the second pore forming domain. The expression of the mutant protein in a cell confers improved inward potassium flux and the ability to grow in the presence of potassium. Mutant proteins and their accreageoning polynucleotide sequences can therefore be used to improve inward potassium flux into cells under acidic conditions by modulating the membrane potential using therapeutic agents. The sequences may be used to develop agonists and antagonists of potassium channel proteins in order to control pests such as nematodes and insects. This sequence represents a human transmembrane potassium ion channel TPKCI mutant
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                                                                                                                                                                                                                                                                                  New polypeptide, a mutant potassium ion channel protein for improving inward potassium flux under acidic conditions.
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                                                                                                                                                                                                                                                                                                                                                                    Claim 37; Page 113-115; 131pp; English
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14-FEB-2001; 2001WO-US004680.
                                                   15-FEB-2000; 2000US-00503849
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                                                                                                                                                                                                            2001-536570/59
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                                                                                                                                                                                                                                       N-PSDB; AAS12181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 426 AA;
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four membrane spanning domains and two pore forming domains, comprising a mutation at the second pore forming domain. The expression of the mutant protein in a cell confers improved inward potassium flux and the ability to grow in the presence of potassium. Mutant proteins and their corresponding polynucleotide sequences can therefore be used to improve inward potassium flux into cells under acidic conditions by modulating the membrane potential using therapeutic agents. The sequences may be used to develop agonists and antagonists of potassium channel proteins in order to control pests such as nematodes and insects. This sequence represents a human transmembrane potassium ion channel TPKCI mutant
GAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 VAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVESDTTINVWKWKTVSTIFLVVVLYLLI 75
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                                                                                                                                                                                                                                                                                                                                                                               Transmembrane potassium ion channel protein; inward potassium flux; pest control; membrane potential; pesticide; antihelminthic; nematode; insect; TPKC1; human; mutant; mutein.
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                                                                                    376 BLTPCRRTLSVNHLTSERDVLPPLLKTESIYLNGLAPHCAGEBIAVIENIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Wild-type Gly replaced by Arg"
                                                                                                                                                                                                                                                                                                                                           Human potassium ion channel TPKC1 mutant protein #4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polypeptide, a mutant potassium ion channel inward potassium flux under acidic conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 37; Page 119-120; 131pp; English.
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                                                                                                                                                                                                                  AAU07625 standard; protein; 426
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                                                                Transmembrane potassium ion channel protein; inward potassium flux; pest control; membrane potential; pesticide; antihelminthic; nematode; insect; TPKC1; human; mutant; mutein.
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                          Human potassium ion channel TPKC1 mutant protein #2.
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                                                                                                                                                                                            Location/Qualifiers
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Matches 390; Conservative
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                                        SNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ
                                                                  SNOISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDO
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used to develop agonists and antagonists of potassium channel proteins order to control pests such as nematodes and insects. This sequence represents a human transmembrane potassium ion channel TPKC1 mutant
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14; Mismatches 8;
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GenCore version 5.1.6
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OM protein - protein search, using sw model

July 13, 2005, 08:01:55; Search time 93.9622 Seconds (without alignments) 2239.886 Million cell updates/sec Run on:

US-09-503-089A-4 2090 1 MAAPDLLDPKSAAQNSKPRL......LNGLTPHCAGEDIAVIENMK 411 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1612378 Total number of hits satisfying chosen parameters:

1612378 segs, 512079187 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	38 mus musculu	og mus musculu	of rattus norv	2 homo sapien	38 bos taurus			oo m mus muscu	vl m mus muscu	34 rattus norv	homo		xenor	18 homo sapien	54 mus musculu	4 rattus norv	m mus	homo	рошо	homo	homo	рошо	brach		52 m potassium		o mus musculu	xeno		рошо	cavia
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SUMMER	OUSE	Q6P6 <u>P</u> 9	Q920B6	_	_	CIW2_HUMAN	Q6Q8 <u>3</u> 4	Q8BZB0	Q8BUW1	CIWA RAT			Q68EY1	CIW4 HUMAN	CIW4_MOUSE	Q924 <u>T</u> 4	Q9CX88		_	_		-	Q6PFU3		Q9JK62	_	Q80XE0	Q801T4	Q8N4V5	CIWH HUMAN	Q8R454
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% Query Match	100.0	99.6	98.6	97.8	97.3	96.2	60.4	60.1	60.1	60.1	59.9	59.9	58.5	38.1	36.9	36.2	29.9	23.9	23.6	23.1	21.7	21.4	20.8	20.1	19.6	19.3		19.3	18.9	18.6	18.0
Score	2090	2082	2061	2044	2034	2011	1261.5	1256.5	1256.5	1256.5	1251.5	1251.5	1223.5	797	770.5	757.5	624	499.5	493.5	482.5	453	447	434.5	420	409	404	403.5	402.5	395	389	377
Result No.		7	٣	4	Ω.	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31

Q99199 mus musculu C00180 homo sapien Q9222 zaturus norv C00581 mus musculu C14649 homo sapien Q8415 xeropus lae C02821 cryctolagus Q94427 homo sapien Q91158 cartu porce Q6peil brachydanio C35111 mus musculu C54912 zattus norv C65210 xenopus lae Q92346 xattus norv	
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ALIGNMENTS

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Similarity
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SEQUENCE FROM N.A.
                                         NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                      Cytoplasmic (Potential).
Essential for chloroform and halothane
                                                                                                                                                                       Potassium channel; Transmembrane; Transport; Voltage-gated channel.
1 46 Cytoplasmic (Potential).
TRANSMEM 47 67 Potential.
                                                                                                                                                                                                                                                                                         Required for basal channel activity.
N-linked (GlCNAc. . ) (Potential).
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                                                            GO; GO:0008076; C:voltage-gated potassium channel complex; IDA. GO; GO:0008076; C:voltage-gated potassium channel activity; IDA. GO; GO:0007186; P:voltage-gated potassium channel activity; IDA. GO; GO:0007813; P:potassium ion transport; IDA. InterPro; IPR003280; K+channel Zpore. InterPro; IPR001622; K+channel Zpore. InterPro; IPR001622; K+channel pore. InterPro; IPR001976; Trek channel. PRINTS; PR01433; 220078KCHANEL.
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                                                                                                                                                                                                                           Cytoplasmic (Potential).
Potential.
Pore-forming 2 (Potential).
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8F976DDD103EFA05 CRC64;
                                                                                                                                                              Glycoprotein; Ion transport; Ionic channel; Potassium;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 2090; DB 1;
100.0%; Pred. No. 4.3e-133;
ive 0; Mismatches 0;
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           entities requires a license agreement (Se or send an email to license@isb-sib.ch).
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                                         EMBL; U73488; AAC53005.2; -.
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Matches 411; Conservative
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Q6P6P9;
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O5-JUL-2004
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Strausberg R.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.

Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.

1. Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.

1. SIMILARITY: Belangs to the two pore domain potassium channel.

(TC 1.A.1.8) family.

R GO 50:0006131 Gintegral to membrane; TAS.

R GO; GO:0006131 Gintegral to membrane; TAS.

R GO; GO:0006135 F:voltage-gated potassium channel activity; IDA.

R GO; GO:0006131 F:voltage-gated potassium channel activity; IDA.

R GO; GO:0006131 F:potassium ion transport; ITAS.

R InterPro; IPR001525; K-thannel_Dore.

InterPro; IPR001525; K-thannel_Dore.

INTERPRO; IPR001525; R-thannel_Dore.

INTERPRO; IPR001525; R-thannel_Lore.

INTERPRO; IPR001525; R-t
                                                                                                                                                                                                                                                                                                             STRAIN-CSTRL/6; TISSUE-Brain;

WEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

A Lischul S.P., Collins F.S., Wanger L., Schaefer C.F., Bhat N.K.,

A Lischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K.F., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

R Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahe J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

""Generation and initial analysis of more than 15,000 full-length human
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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SEQUENCE 414 AA; 45555 MW; 27F52D51DFFC66F8 CRC64;
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Pred. No. 1.5e-132;
1; Mismatches 1;
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ilarity 99.5%;
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TISSUB-PCR rescued clones;

TISSUB-PCR rescued clones;

MEDINEE-218825;

PUBLINEE-218825;

PUBLINEE-21
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76 GATVFKALEQPQEISQRTTIVIQKQNFIAQHACVNSTELDELIQQIVTAINAGIIPLGNN 135
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
25-OCT-2004 (TrEMBLrel. 26, Last annotation update)
Two-pore domain potassium channel TREK-1 (Potassium channel, subfamily
                                                                                                     136 SNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLAGVGDQ
                                                                                                                                                                                                                                      196 LGTIFGKGIAKVEDTFIKWNVSQTKIRISTIIFILFGCVLFVALFAVIFKHIEGWSALD
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                                                                                                                                                                                                181 LGTIFGKGIAKVEDTFIKMNVSQTKIRIISTIIFILFGCVLFVALPAVIFKHIEGWSALD
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                                                                  SNOVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDO
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1. Acad. Sci. U.S.A. 99:16899-16903(2002)
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MEDLINE=20244931; PubMed=10784345;
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Homo sapiens (Human).
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SEQUENCE FROM N.A.
TISSUE=PCR rescued clones;
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244 AIYFVVITLTIGFGDYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS 303
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Karschin A., Derst C., Steinlein O.K., Daut J.;
"Expression pattern and functional characteristics of two novel splice
variants of the two-pore-domain potassium channel TREK-2.";
J. Physiol. 539:657-668(2002).
                                                                                                     KKTKEEVGEFRAHAAEWTANVTAEFKETRRLSVBIYDKFQRATSVKRKLSAELAGNHNQ
                                                                  KKTKEEVGEFRAHAAEWTANVTAEFKETRRLSVEIYDKFQRATSVKRKLSAELAGNHNQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
27-OCT-2004 (TrEMBLrel. 28, Last annotation update)
29 domain potassium channel KCNK2 (Tandem pore domain channel TREK-1) (Arachidonic acid sensitive tandem pore domain
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MEDLINE=21896087; PubMed=11897838;
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Matches 404; Conservative
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16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
botassium channel subfamily K member 2 (Outward rectifying potassium channel protein TREK-1) (TREK-1 K+ channel subunit) (Two-pore
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SEQUENCE FROM N.A.
SEQUENCE PROM N.A.
MEDLINE=99254548; PubMed=10321245; DOI=10.1038/8084;
MEDLINE=992554548; PubMed=10321245; Fink M., Romey G., Lazdunski M.;
Patel A.J., Honore E., Lessage F., Fink M., Romey G., Lazdunski M.;
"Inhalational anesthetics activate two-pore-domain background K+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Wasaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                               TC 1.A.1.8 family.

REBL; AV148474; AAN37591.1; -.

REBL; AV148474; AAN37591.1; -.

RGG; GO:0016021; C:integral to membrane; IEA.

RGG; GO:0016021; C:integral to membrane; IEA.

RGG; GO:0005216; F:ion channel activity; IEA.

RGG; GO:0006811; P:ion transport; IEA.

RGG; GO:0006813; P:potassium ion transport; IEA.

RGG; GO:0006813; P:potassium ion transport; IEA.

RICHEPTO; IPR001622; K+channel_2pore.

InterPro; IPR001622; K+channel_2pore.

InterPro; IPR001996; Trek_channel.

RRINTS; PR0133; 2POREKCHÄNEL.

RRINTS; PR01499; TREKCHÄNNEL.

RENUTS; PR01499; TREKCHÄNNEL.

RINTS; PR01499; TREKCHÄNNEL.

REQUENCE 411 AA; 45438 MW; A185EAC20A68CCDC CRC64;
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96.1%; Pred. No. 2.6e-129;
ive 10; Mismatches 6;
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277:49186-49199(2002).
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Name=KCNK2; Synonyms=TREK, TREK1;
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[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSIKRKLSAELAGNHNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVVLYLII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAIIFKHIEGWSALD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS
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TISSUB=Adrenal cortex;
MEDLINE=22370953; PubMed=12368289; DOI=10.1074/jbc.M207233200;
Enyeart J.J., Xu L., Danthi S., Enyeart J.A.;
"An ACTH- and ATP-regulated background K+ channel in adrenocortical cells is TREK-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name-Kcnk2;
bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                    Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.8) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         411
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                                                                                                                                                                                                                                                                                                                                                                                                                      Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                    Ion transport; Ionic channel; Transmembrane; Transport
SEQUENCE 411 AA; 45494 MW; FDE40CAB21B42A1C CRC64;
                                                                             EMBL; AF171068; AAF89743.1; -.
EMBL; BC069462; AAF89743.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0005216; F:ion channel activity; IEA.
GO; GO:0005216; F:ion channel activity; IEA.
GO; GO:0006211; F:ion transport; IEA.
GO; GO:0006813; P:potassium ion transport; IEA.
InterPro; IPR003280; K+channel_zpore.
InterPro; IPR001622; K+channel_zpore.
InterPro; IPR001622; K+channel_pore.
InterPro; IPR01333; ZPOREKCHANEL.
PRINTS; PR01333; ZPOREKCHANEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Potassium channel subfamily K member 2.
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 97.8%; Score 2044; DB 2;
Best Local Similarity 96.4%; Pred. No. 5.5e-130;
Matches 396; Conservative 11; Mismatches 4;
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316 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSIKRKLSAELAGNHNQ 375
                                                            256 AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGRLVRVIS 315
                                                                                                                  KKTKEEVGEFRAHAAEWTANVTAEFKETRRLSVEIYDKFQRATSVKRKLSAELAGNHNQ 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 YLIIGAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIP 116
196 LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAIIFKHIEGWSALD 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSV----KRKLS 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAPDLLDPKSAAQN--SKPRLSFSSKPTVLASRVESDS---AINVMKWKTVSTIFLVVVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAPPVCQPKSATNGHPAAPRLSISSRATVVA-RMEGTSQGGLQSVMKWKTVVAIFVVVVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 LGNSSNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAVIFKHIEGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SALDAIYFVVITLTTIGFGDYVAGG-SDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rea J.L.;
Submitted (PEB-2004) to the EMBL/GenBank/DDBJ databases.

Submitted (PEB-2004) to the two pore domain potassium channel -1- SIMILARITY: Belongs to the two pore domain potassium channel -1- SIMILARITY: Belongs to the two pore domain potassium channel -1- SIMILARITY: Belongs to the two pore domain potassium channel -1- SIMILARITY: BEA.

Red, 60:0016216; F:ion channel activity; IEA.

Red); GO:0006211; F:ion transport; IEA.

Red); GO:0006811; P:ion transport; IEA.

Red); GO:0006811; P:ion transport; IEA.

Red); GO:0006813; P:potassium ion transport; IEA.

InterPro; IPR0012280; K-channel pore.

InterPro; IPR001329; Trek_channel.

Red RINTS; PR01333; ZPOREKCHANNEL.

RENINTS; PR01499; TREKCHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                      376 ELTPCRRTLSVMHLTSERDVLPPLLKTESIYLNGLAPHCAGEEIAVIENIK 426
                                                                                                                                                                                                 361 ELTPCRRTLSVNHLTSEREVLPPLLKAESIYLNGLTPHCAGEDIAVIENMK 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ion transport; Ionic channel; Transmembrane; Transport
SEQUENCE 538 AA; 59844 MW; 1F06C8EA0DE8CB4D CRC64;
                                                                                                                                                                                                                                                                                                                                                                            05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 4.9e-77
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                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Potassium channel TREK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 247; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9986;
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                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@iBb-sib.ch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 GATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQIVAAINAGIIPLGNT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGTIFGKGIAKVEDTFIKWNSQTKIRIISTIIFILFGCVLFVALPAVIFKHIEGWSALD 240
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                               16 VAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVVLYLII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0015271; F:outward rectifier potassium channel activity; NAS.
GO; GO:0006813; P:potassium ion transport; NAS.
InterPro; IPR003280; K+channel_pore.
InterPro; IPR001622; K+channel_pore.
InterPro; IPR0016376; Trek channel.
PRINTS; PR01333; 2POREKCHĀNEL.
PRINTS; PR01499; TREKCHĀNBEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Počasšium channel, Transmembrane, Transport, Voltage-gated channel. DOMAIN 1 61 Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Binilarity.)
N-linked (GlcNAc. . .) (Potential).
N-linked (GlcNAc. . .) (Potential).
Missing (in Ref. 2).
RLV -> DM (in Ref. 2).
S -> N (in Ref. 2).
A -> T (in Ref. 2).
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Pore-forming 1 (Potential).
Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Potential.
Pore-forming 2 (Potential)
Potential.
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95.1%; Pred. No. 9.7e-128;
iive 13; Mismatches 7;
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Best Local Similarity 95.14
Matches 391; Conservative
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MIM; 603219; -.
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LRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATIRSMERRLG 381
                                                                                                                                                                                                                                                                                                                                                                            Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:9630032C21 product:POTASSIUM CHANNEL SUBFAMILY K MEMBER 10 (OUTWARD RECTIFYING POTASSIUM CHANNEL PROTEIN TREK-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/63; TISSUB=Cerebellum; MEDLINE=20499374; Pubmed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libaries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CSTBL/60; TISSUE=Cerebellum;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Rayashizaki Y.;
High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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MEDLINE=CS7BL/GJ; TISSUB=Cerebellum;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINE=20530913; PubMed=110.7 Nishi K., Riteunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Matahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Mashiwayi K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Masuura S., Kawai J., NikEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Functional annotation of a full-length mouse cDNA collection.";
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Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Ca:
Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
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MEDLINE-21085660; PubMed=11217851; DOI=10.1038/35055500;
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The FANTOM Consortium,
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                                                                                352 AELAGNHNQELTPCRRTL 369
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Nature 420:563-573(2002).
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Mus musculus 0 day neonate creebellum cDNA, RIKEN full-length enriched
library, clone:C230015H11 product:POTASSIUM CHANNEL SUBFAMILY K MEMBER
10 (OUTWARD RECTIFYING POTASSIUM CHANNEL PROTEIN TREK-2) (TREK-2 K+
CHANNEL SUBUNIT) homolog.
Mus musculus (Mouse).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Rotch H., Kawai J., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S. Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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LDQRAHSLDMLSPEKRSV 396
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Matches 247; Conservative
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Q9JIS4;
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Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Pukuda S., Puruno M., Hangaki T., Haraoka T., Hackane T.,
Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
Hori R., Imotani K., Ishii Y., Itoh M., Kagawa I., Kauwa T.,
Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Koda M., Koya S.,
Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Koda M., Koya S.,
Kurihara C., Matsuyama T., Myazaki A., Murata M., Nakamura M.,
Nishi K., Saitoh H., Sakai C., Sakai K., Sakazuwa N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tagami M.,
Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
Submitted (ARR-2002) to the EWBL/Genbank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A..
STRAINE-STBL/GJ; TISSUE=Cerebellum;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
Manalysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Muramatsu M., Hayashizaki Y.; Itoh M., Phayashizaki Y.; Pubraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                          STRAIN=C57BL/6J; TISSUE=Cerebellum;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CSTBL/61; TISSUE=Cerebellum;

MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsunnoto H., Sakaguchi S., Ikegami T., Kashiiwagi K.,
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiayaj K.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RIKEN integrated sequence analysis (RISA) system-384-format
Sequencing pipeline with 384 multicapillary sequencer.";
Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
                                                                                                                                                                                                                                                                           annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                             STRAIN=CS7BL/67; TISSUE=Cerebellum;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AK082153; BAG38424.1; -. GO; GO:0016021; C:integral to membrane; IEA. GO; GO:0005216; F:ion Channel activity; IEA. GO; GO:0005267; F:potassium channel activity; IEA. GO; GO:0006811; P:ion transport; IEA. GO; GO:0006813; P:potassium ion transport; IEA.
                                                                                                                   Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
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InterPro, IPR001622, K+channel pore.
InterPro, IPR003976; Trek_channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Cerebellum;
                                                                                                                                                          Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                  Nature 409:685-690(2001).
                                                                                                                                                                                                                                                           RIKEN FANTOM Consortium;
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                                                                                                                                                                                                                           20 AAPPVCQPKSATNGHHPVPRLSISSRATVVA-RMEGASQGGLQTVMKWKTVVAIFVVVVV 78
                                                                                                                                                                                                 2 AAPDLLDPKSA--AQNSKPRLSFSSKPTVLASRVESDS---AINVMKWKTVSTIFLVVVL
                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Potassium channel subfamily K member 10 (Outward rectifying potassium channel TREK-2) (TREK-2 K+ channel subunit).
                                                                                                                                                                                                                                                                                                                                                                               117 LGNSSNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 VGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAVIFKHIEGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SALDAIYFVVITLTTIGFGDYVAGG-SDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDW
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Bang H., Kim Y., Kim D.;
Rang H., Kim Y., Kim D.;
"TREK-2, a new member of the mechanosensitive tandem-pore K+ channel
"TREK-2, a new member of the mechanosensitive tandem-pore K+ channel
"TREK-2, a new member of the mechanosensitive tandem-pore K+ channel
"TREK-2, a new member of the mechanosen K+ channel
"TONGTION: Outward rectifier K(+) currents
activating and non-inactivating outward rectifier K(+) currents
Activated by arachidonic acid and other naturally occurring
unsaturated free fatty acids.
-: SUBCELDULAR LOGATION: Integral membrane protein (Potential).
-: TISSUE SPECIFICITY: Expressed mainly in the cerebellum, spleen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Mětazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                        11;
                                                                                                          Length 535;
                                                                                                                                                      65; Indels
                                         Ion transport; Ionic channel; Transmembrane; Transport SEQUENCE 535 AA; 59401 MW; 3E98E89F875C26BD CRC64;
                                                                                                            DB 2;
                                                                                                       60.1%; Score 1256.5; DB 65.3%; Pred. No. 1.1e-76; ive 55; Mismatches 65
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PRINTS; PR01333; 2POREKCHANEL.
PRINTS; PR01499; TREKCHANNEL.
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                                                                                                       Query Match
Best Local Similarity 65.34
Matches 247; Conservative
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and for commercial
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                                                                                                                                                                                                                                                                                 23 AAPPVCQPKSATNGHHPVPRLSISSRATVVA-RMEGASQGGLQTVMKWKTVVAIFVVVVV 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS7789; QBTDK7; QBTDK8; Q9HB59; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 05-UUL-2004 (Rel. 44, Last annotation update) Potassium channel subfamily K member 10 (Outward rectifying potassium channel TREK-2) (TREK-2 K+ channel subunit).
                                                                                                                                                                                                                                                                                                                                                237 SALDAIYFVVITLTTIGFGDYVAGG-SDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDW
                                                                                                                                                                                                                                                                                                                                                                                                                       2 AAPDLLDPKSA--AQNSKPRLSFSSKPTVLASRVESDS---AINVMKWKTVSTIFLVVVL
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                                                                                                                                                                                                                                               Gaps
                                                                                                Transmembrane, Transport, Voltage-gated channel
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
[1]
                                                                                                                                                                       Potential.
Cytoplasmic (Potential).
N-linked (GLONAc. . ) (Potential).
                                                                                                                                                                                                           Pore-forming 1 (Potential). Potential.
                                                                                                                                             Cytoplasmic (Potential).
Potential.
Pore-forming 2 (Potential).
Usage by
                                                                                        Glycoprotein; Ion transport; Ionic channel; Potassium; Potassium; channel; Transport; Voltage-g
                                                                                                                                                                                                  -linked (GlcNAc. . .) (P. IFF33F0AA52B97E4 CRC64;
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modified and this statement is not removed.
                                                                                                                                                                                                                             65.3%; Score 1256.5; 65.3%; Pred. No. 1.1e
         entities requires a license agreement (or send an email to license@isb-sib.ch)
                                  EMBL, AF196965; AAF75132.1; -.
InterPro; IPR003280; K+channel_2pore.
InterPro; IPR001622; K+channel_pore.
InterPro; IPR003976; Trek_channel.
PRINTS; PR01333; 2POREKCHANEL.
PRINTS; PR01499; TREKCHANNEL.
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                                                                                                                                                                                                            59800 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=KCNK10; Synonyms=TREK2;
Homo sapiens (Human).
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538 AA;
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nes 247; Conserv
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RP SEQUENCE FROM N.A. (ISOFORMS B AND c).

RP SEQUENCE FROM N.A. (ISOFORMS B AND c).

RA MEDLINE=21896087; PubMed=11897838;

RA Gu W., Schlichthorl G., Hirsch O.R., Baut J.;

RA Farschin A., Derst C., Steinlein O.K., Daut J.;

RA Farschin A., Derst C., Steinlein O.K., Daut J.;

RA Farschin A., Derst C., Steinlein O.K., Daut J.;

RY "Expression pattern and functional characteristics of two novel splice

RY "Expression pattern and functional potassium channel TREK-2.";

RI J. Physiol. (Lond.) 539:657-668(2002).

C. - I- PUNCTION: Outward rectifitying potassium channel. Produces rapidly activating and non-inactivating outward rectifier K(+) currents.

CC Activating and non-inactivating outward rectifier K(+) currents.

CC Activating and non-inactivating outward rectifier K(+) currents.

CC Activated free fatty acids.

CC -- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

CC -- ALTERNATIVE PRODUCTS:

CC -- ALTERNATIVE PRODUCTS:

CC -- ALTERNATIVE SPRICING: Named isoforms=3;

N=me=A: Synonyms=TREK-2a;

N=me=A: Synonyms=TREK-2a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
B-FLYTDFFLSL -> MKGDRTEGCRSDS (in isoform B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=A: Synonyms=TREK-2a;
IsoId=P57789-1; Sequence=Displayed;
Name=B: Synonyms=TREK-2b;
Name=C: Synonyms=TREK-2c;
Name=C: Synonyms=TREK-2c;
IsoId=P57789-2; Sequence=VSP_006698;
IsoId=P57789-3; Sequence=VSP_006698;
TISSUE SPECIFICITY: Abundantly expressed in pancreas and kidney and to a lower level in brain, testis, colon, and small intestine.
Isoform b is strongly expressed in kidney (primarily in the proximal tubule) and pancreas, whereas isoform c is abundantly
                                                                                                                         gg
                                                                                           multiple
                                                    Lesage F., Terrenoire C., Romey G., Lazdunski M.;
"Human TREKZ, a 2P domain mechano-sensitive K+ channel with multip
regulations by polyunsaturated fatty acids, lysophospholipids and id, and Gq protein-coupled receptors.";
J. Biol. Chem. 275:28398-28405(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alternative splicing; Glycoprotein; Ion transport; Ionic channel; Potassium; Potassium channel; Transmembrane; Transport; Voltage-gated channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Expressed in brain. SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.8) family.
SEQUENCE FROM N.A. (ISOFORM A).
MEDLINE=20435789; PubMed=10880510; DOI=10.1074/jbc.M002822200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pore-forming 2 (Potential). Potential.
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GO; GO:0005267; F:potassium channel activity; TAS.
GO; GO:0006810; P:transport; TAS.
InterPro; IPR0013280; K+channel_zpore.
InterPro; IPR001522; K+channel_pore.
InterPro; IPR001956; Trek-channel.
PRINTS; PR01333; 2POREKCHĀNEL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         290 SMIGDWLRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRLSVEIYDKFQRATSV--- 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                321 SMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATIRSM 380
Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 FLVVVLYLIIGAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 NAGIIPLGNSSNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 AAAPVCQPKSAINGQPPAPAPIPIPRISISSRAIVVA-RMEGISQGGLQIVMKWKIVVAI
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Amphibia; Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
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                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC075021; AAH75021.1; -
EMBL; BC075021; AAH75021.1; -
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005267; F:gon channel activity; IEA.
GO; GO:0005267; F:gotassium channel activity; IEA.
GO; GO:0006813; P:gotassium ion transport; IEA.
InterPro; IPR003280; K+channel_Zpore.
InterPro; IPR0142125; Nt. SiRAlpha 1/3.
InterPro; IPR0142125; Nt. SiRAlpha 1/3.
InterPro; IPR003976; Trek_channel_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             543 AA; 60110 MW; 17DB1AFAFAB07C46 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kenopus laevis (African clawed frog).
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Matches 247; Conservative
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SEQUENCE FROM N.A.
TISSUE=Pooled tissue;
Director MGC Project;
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Q68EY1
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    RATTA SERVICE 
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TISSUE-Pooled tissue;

MEDINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

X RELINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A platchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Raha S., Warzy D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahay J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schnutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FLVVVLYLIIGAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
/FIId=VSP_006697.
MFFLYTDFFLSL -> MKFPIETPRKQVNWDPK
                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
                                                                                                                                                                                                                                                                                                                               59.9%; Score 1251.5; DB 1; Length 64.3%; Pred. No. 2.3e-76; rive 54; Mismatches 66; Indels
                                                                                              isoform C).
/FTId=VSP_006698.
E -> G (in Ref. 2).
8EA615B08D147FBC CRC64;
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Potassium channel, subfamily K, member 10, isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
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59764 MW;
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28,
28,
                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 64.3
Matches 247; Conservative
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25-OCT-2004 (TrEMBLrel.
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                                                      VARSPLIC
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PubMed=12477932; DOI=10.1073/pnas.242603899;

Ratausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Ratausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Ratausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Ratachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninoi P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Raha S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Shevchenko Y., Bouffard G.G.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Ratagesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Jones S.J., Marra M.A.,

Jones S.J., Marra M.A.,

Rad Generation and initial analysis of more than 15,000 full-length human med mouse CDNA sequences.",
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         257 YVAGG-SDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVISKKTKEEVGEFRAHAA 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
              MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                               'Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60977 MW; AF6C7FB34AD34A06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58.5%; Score 1223.5; DB ; 60.6%; Pred. No. 1.8e-74; iive 62; Mismatches 70;
                                                                                                  Dyn. 225:384-391(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 60.6
nes 241; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   546 AA;
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                                                                                    initiative.'
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PERIOR ISOPORM(S) THAT ARE POTENTIAL NWD TARGET(S).

RA Hillman R.T., Green R.E., Brenner S.E.;

"An unappreciated role for RNA surveillance.";

The number of the for RNA surveillance.";

Genome Biol. 5:RESEARCH008.1.RESEARCH008.16(2004).

-I- FUNCTION: Voltage insensitive, instantaneous, outwardly rectifying potassium channel. Outward rectification is reversed at high external K(+) concentrations [By similarity).

-I- SUBCELLUAR LOCATION: Integral membrane protein (Potential).

-I- ALTERNATUR PRODUCTS:

-I
                                                                                                                                                                                                                                                            16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2004 (Rel. 44, Last amoutation update)
05-UUL-2004 (Rel. 44, Last annotation update)
Potassium channel subfamily K member 4 (TWIK-related arachidonic acid-stimulated potassium channel protein) (TRAAK) (Two pore K+ channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=20231699; PubMed=10767409; DOI=10.1016/S0014-5793(00)01388-0;
Lesage F., Maingret F., Lazdunski M.;
Loning and expression of human TRAAK, a polyunsaturated fatty acids-
activated and mechano-sensitive K(+) channel.";
FEBS Lett. 471:137-140(2000).
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MEDLINE=22178385; PubMed=12191490; DOI=10.1016/S0169-328X(02)00157-2;
Ozaita A., Vega-Saenz de Miera E.;
"Cloning of two transcripts, HTV4.1a and HKT4.1b, from the human two-pore K+ channel gene KCNK4. Chromosomal localization, tissue distribution and functional expression.";
Exain Res. Mol. Brain Res. 102:18-27(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=11142359; DOI=10.1016/80169-328X(00)00183-2; Chapman C.G., Meadows H.J., Godden R.J., Campbell D.A., Duckworth M., Kelsell R.E., Murdock P.R., Randall A.D., Rennie G.I., Gloger I.S.; "Cloning, localisation and functional expression of a novel human, cerebellum specific, two pore domain potassium channel."; Brain Res. Mol. Brain Res. 82:74-83(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Assignment of KCNK4 encoding the human potassium channel TRAAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Curromosome ii. ,
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
394
                                                       ELEAGREKASSODSINNRPNNLR----LKEAEQFTLHG 445
------SVNHLTSEREVLPPLLKAESIYLNG
                                                                                                                                                                                                        393 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=KCNK4; Synonyms=TRAAK;
                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Frontal cortex;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Brain;
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                                                          412
370
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4 (TWIK-related arachidonic acid-

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channels.";
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CARBOHYD
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VARSPLIC
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  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the RMBL outstation - the European Bioinformatics. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a alicense agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibs-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240
                                                                                                                                                                                                                                                                                                                                                                                                                                                           42 MKWKTVSTIFLVVVLYLIIGAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDE 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 LIQQIVAAINAGIIPLGNSSNQVSH--WDLGSSFFFAGTVITTIGFGNISPRTEGGKIFC 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                220 VLFVALPAVIFKHIEGWSALDAIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWIL. 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160 IIYALLGIPLFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                              MIM, 605720; -...
GO: GO:00056813; P:potassium channel activity; TAS.
GO: GO:0006813; P:potassium ion transport; TAS.
GO: GO:0006813; P:potassium ion transport; TAS.
InterPro; IPR003280; K+channel_pore.
InterPro; IPR001622; K+channel_pore.
InterPro; IPR008044; TRAAK channel.
PRINTS; PR01331; 2POREXCHANEL.
PRINTS; PR01591; TRAAKCHANEL.
Alternative splicing; Glycoprotein; Ion transport; Ionic channel;
Potassium; Potassium channel; Transmembrane; Transport;
                                                                                                                                                                                                                                                                                                                                                       M -> MTTAPQEPPARPLQAGSGAGPAPGRAM (in
                                                                                                                                                                                                                                                                                                                          Cytoplasmic (Potential).
N-linked (GlCNAc. . .) (Potential).
N-linked (GlCNAc. . .) (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 393;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77; Indels
                                                                                                                                                                                                                                                                                   Cytoplasmic (Potential), Potential.
Pore-forming 2 (Potential).
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P -> L (in Ref. 2).
7F18E53A0A9AD57D CRC64;
                                                                                                                                                                                                                                           Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                  38.1%; Score 797; DB 1;
51.1%; Pred. No. 8.1e-46;
iive 60; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                  Potential.
                                                                                                                                                                                                                                                                                                                                                                   isoform 2
                                                                             EMBL, AF248242; AAG31731.1; -.
EMBL, AF247042; AAF64062.1; ALT_INIT.
EMBL, APZ59500; AAK49389.1; -.
EMBL, AFZ59501; AAK49390.1; -.
Genew, HGNC:6279; KCNK4.
                                                                                                                                                                                                                                                                                                                                                                                                 42704 MW;
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Matches 145; Conservative 6
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1113
1138
1171
1192
221
2254
3393
78
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393 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                89
1118
139
172
197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CIW4 MOUSE
088454;
16-0CT-2001
16-0CT-2001
05-JUL-2004
                                                                                                                                                                                                                                                                                     DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                                                                                                    CARBOHYD
CARBOHYD
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        280
                                                                                                                                                                                                                                                     TRANSMEM
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                                                                                                                                                                                                                                                                                                                  RANSMEM
                                                                                                                                                                                                                                                                 DOMAIN
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CIW4_MOUSE
                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                             DOMAIN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MISCELLANDEOUS: Activated by arachidonic acid and other unsaturated fatty acids. Not affected by volatile general anaesthetics such as chloroform, diethyl ether, halothane and isoflurane.
SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.8) family.
                                                                                                                                                                                                                                                                                                                                                                                                                              "A neuronal two P domain K+ channel stimulated by arachidonic acid and polyunsaturated fatty acids.";
EMBO J. 17:3297-3308(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- FUNCTION: Voltage insensitive, instantaneous, outwardly rectifying potassium channel. Outward rectification is reversed at high external K(+) concentrations.
-i- SUBGUNIT: Homodimer (Potential).
-i- SUBGELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isoid=088454-1; Sequence=Displayed;
Name=2; Synonyms=TRAAKT, Truncated;
IsoId=088454-2; Sequence=VSP 006690, VSP 006691;
TISSUE SPECIFICITY: Expressed in brain, spinal cord and eye. Not detected in heart, skeletal muscle, liver, lungs, kidney and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTIVATION.
MEDLINE-99254548; PubMed=10321245; DOI=10.1038/8084;
Patel A.J., Honore B., Lesage F., Fink M., Romey G., Lazdunski M.;
"Inhalational anesthetics activate two-pore-domain background K+
                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                 MEDLINE-98292450; PubMed-9628867; DOI=10.1093/emboj/17.12.3297;
Fink M., Lesage F., Duprat F., Heurteaux C., Reyes R., Fosset M.,
Lazdunski M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       channel;
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N-linked (GlcNAc. . ) (Potential)
N-linked (GlcNAc. . ) (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLLVE -> KAMAI (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:1298234; Kcnk4.
InterPro; IPR001280; K+channel_pore.
InterPro; IPR001280; K+channel_pore.
InterPro; IPR001622; K+channel_pore.
InterPro; IPR001632; K+channel.
PRINTS; PR0133; 2POREKCHANEL.
PRINTS; PR01591; TRAAKCHANEL.
Alternative pplicing; Glycoprotein; Ion transport; Ionic Potassium; Potassium channel; Transmembrane; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pore-forming 1 (Potential). Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pore-forming 2 (Potential). Potential.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=2;
Potassium channel subfamily K member 4 (TWIK-:
stimulated potassium channel protein) (TRAAK)
Name=Kcnk4; Synonyms=TRAAK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF056492; AAC40181.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nat. Neurosci. 2:422-426(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Voltage-gated channel
DOMAIN
                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140
172
198
235
256
81
81
63
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1;
                                                                                                        42 MKWKTVSTIFLVVVLYLIIGAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDE 101
                                                                                        9
                                                                                 3; Gaps
                                       Query Match 36.9%; Score 770.5; DB 1; Length 398; Best Local Similarity 49.8%; Pred. No. 5.1e-44; Matches 142; Conservative 56; Mismatches 84; Indels 3.
                                                                                                                                                                                                        /FTId=VSP 006690.
68 398 Missing (In isoform 2).
//FIG=VSP 006691.
398 AA, 43051 NW, 478A834B7B7AEC92 CRC64;
                        SEQUENCE
        VARSPLIC
FFFS
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Search completed: July 13, 2005, 08:44:31 Job time : 95.9622 secs

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GenCore version 5.1.6

Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

July 13, 2005, 08:02:40 ; Search time 21.6316 Seconds

(without alignments)

1828.118 Million cell updates/sec
```

Title: Perfect score: Sequence:	US-09-503-089A-4 2090 1 MAAPDLLDPKSAAQNSKPRLLNGLTPHCAGEDIAVIENMK 411
Scoring table: BLOSUM62 Gapop 10	BLOSUM62 Gapop 10.0 , Gapext 0.5
Searched:	283416 segs, 96216763 residues
Total number o	Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	inward rectifier p	TASK-5 protein - h	probable potassium	outward rectifier	potassium channel	hypothetical prote	hypothetical prote	probable potassium	potassium channel	hypothetical prote			hypothetical prote	O,	hypothetical prote				_			hypothetical prote	probable potassium	hypothetical prote			hypothetical prote	outward-rectifier	hypothetical prote
SUMMARIES	ΩI	865566	JC7703	T43509	T32347	T13807	T23182	T19860	T43361	T43394	T25392	T45032	T24265	T15584	H88124	T21118	T30037	T26229	T28933	T27681	T26616	T22557	T23907	T43529	T16629	T21834	T21598	T26953	S46585	T16426
	8	~	~	~	~	~	N	7	~	~	N	~	~	•	•	N					~	0	~	~						
	Length	336	330	329	336	1001	383	334	364	461				325	1910	452	1539	444	513	427	643			484	519	528	443	1136	691	551
م د	Match	18.0	16.8	16.4	15.8	15.6	13.8	13.7	13.7		13.3	13.0	12.9	12.9	12.7	12.6	12.1	11.8	11.7		11.3	11.3	11.1	11.0	11.0	11.0	10.6	10.5	10.4	10.4
	Score	376.5	351.5	343	329.5	325	289	286.5	286.5	279.5	279	271	270.5	269	266	263	252.5	247	245.5	4	237	236	231	229.5	N	229	221	219	-	216.5
	Kesuir No.	-	7	m	4	S	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	. 25	56	27	28	29

RESULT 2
JC7703
JC7703
JC7703
JC5704
Species: Home sapiens (man)
C;Species: Home sapiens (man)
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C;Accession: JC7703
Biochem. Biophys. Res. Commun. 284, 923-930, 2001
A;Title: TASK-5, a new member of the tandem-pore K+ channel family.
A;Reference number: JC7703; MUID:21303050; PMID:11409881

potassium channel hypothetical prote	f22b7.7 protein -	procein cwk-z4 lim hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	potassium channel	potassium channel	hypothetical prote	hypothetical prote	hypothetical prote	probable potassium	potassium channel
T43357 T27725	844635	T24201	T21683	T21551	T27364	T23373	T43364	T43363	T27550	T23700	T19429	T43531	T43393
00	~ ~	v 0	~	~	~	~	N	N	~	(7	~	~	~
555 475	335	485 485	286	099	700	523	544	576	169	539	. 681	269	381
10.4	10.3	10.1	10.0	ø.	9.6	9.8	9.6	9.6	9.7	9.5	9.4	9.3	9.5
216.5 · 216	215.5	212	209.5	206.5	205	204.5	204.5	204.5	202.5	199.5	196.5	194.5	192.5

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RESULT 1 S65566

inward re C;Species C;Date: 2	inward rectifier potassium channel TWIK-1 - human C.Species: Homo sapiens (man) C.Species: Se Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
R, Lesage, EMBO J. 1	Ribesge, F.; Gullemare, E.; Fink, M.; Duprat, F.; Lazdunski, M.; Romey, G.; Barhanin, EMBO J. 15. 1004-1011. 1996
A;Title:	A:Title: TWIK-1, a ubiquitous human weakly inward rectifying K(+) channel with a novel A:Reference number: 865566: MIID:96183184: PMID:8605869
A; Accessi	A;Accession: S65566
A;Status: A;Molecul	A;Status: preliminary A;Molecule type: mRNA
A;Residue A;Cross-r	A;Residues: 1-336 <les> A;Cross-references: UNIPROT:000180; EMBL:U33632; NID:g1086490; PIDN:AAB01688.1; PID:g10</les>
Query N	Query Match 18.0%; Score 376.5; DB 2; Length 336;
Matches	ocal Similaricy 34.5%; Fred. No. 6.36-23; 3 90; Conservative 62; Mismatches 108; Indels 17; Gaps 9;
ò	51 FLVVVLYLIIGAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVA 108
QQ	25 FLVLGYLLYIVFGAVVFSSVELPYEDLLRQELRKLKRRFLEEHECLSEQQLEGFLGRVLE 84
è	109 AINAGIIPLGNSSNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIP 168
qa	85 ASNYGVSVLSNASGN-WNWDFTSALFFASTVLSTTGYGHTVPLSDGGKAFCIIYSVIGIP 143
ò	169 LFGFLLAGVGDQLGTIFGKGIAKVEDTFIKMNVSQTKIRIISTIIFILFGCVLFVALP 226
qa	144 FTLLFLTAVVQRITVHVTRRPVLYFHIRWGFSKQVVAIVHAVLLGFVTVSCFFFIP 199
ò	227 AVIFKHIE-GWSALDAIYFVVITLTIGFGDYVAG-GSDIEYLDFYKPVVWFWILVGLAY 284
qq	200 AAVESVLEDDWNFLESFYFCFISLSTIGLGDYVFGEGYNQKFRELYKIGITCYLLLGLIA 259
ò	285 FAAVLSMIGDWLRVISKKTKEEVGEFRAHAAE 316
qq	260 MLVVLETFCE-LHELKKFRKMFYVKKDKDEDQVHIIE 295

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potassium channel protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T13807
R;Goldstein, S.A.; Price, L.A.; Rosenthal, D.N.; Pausch, M.H.
Proc. Natl. Acad. Sci. U.S.A. 93, 13256-13261, 1996
A;Title: ORKI, a potassium-selective leak channel with two pore domains cloned from Droc. A;Reference number: Z17770; MUID:97075152; PMID:8917578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: UNIPROT: Q94526; EMBL: U55321; NID: g3808067; PID: g3808068; PIDN: AAC692
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:O17185; EMBL:AF025454; PIDN:AAC71151.1; GSPDB:GN00020; CESP:
A;Experimental source: strain Bristol N2; clone F34D6
C;Genetics:
150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 MTDAGKVFCMLYALAGIPLGLIMFQSIGERMNTFAAKLL----RFIRRAAGKOPIVTSS 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                        outward rectifier potassium channel homolog twk-23 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004 C;Accession: T32347 J.; Wohldmann, P.; O'Neal, D. Bubmitted to the EMBL Data Library, September 1997 A;Pescription: The sequence of C. elegans cosmid F34D6.
A;Reference number: Z1153
A;Accession: T33347
A;Gettus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-336 <MUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIIFILFGC-VLFVALPAVIFKHIEGWSALDAIYFVVITLTTIGFGDYVA---GGS---D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 CVNSTELDELIQQIVAAI --NAGIIPLGNSSNQVSHWDLGSSFFFAGTVITTIGFGNISP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 RTEGGKIFCIIYALLGIPLFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   264 IEYLDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVISKKTKEE 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Introns: 44/3; 102/1; 136/1; 180/1; 207/1; 265/2; 296/3
                                                                                                            223 SLV---FILFGLTVISAAMNLL--VLRFLTMNTEDE 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.8%; Score 329.5; DB 2; 33.2%; Pred. No. 4.1e-19; tive 53; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42 MKWKTVSTIFLVV--VLYLIIGAAVFKALEQPQEISQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Status: preliminary, translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
                                                                                271 KPVVWFWILVGLAYFAAVLSMIGDWLRVISKKTKEE
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A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: twk-23; CESP: F34D6.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 94, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Map position: 2
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     A;Molecule type: DNA
A;Residues: 1-330 <KIM>A;Residues: 1-330 <KIM>A;Residues: 1-330 <KIM>A;Residues: 1-330 <KIM>A;Residues: 1-330 <KIM>A;Residues: 1-330 <KIM>A;Crosa-references: GB-ALI1852
C;Comment: This protein, a new member of the tandem-pore K+ channel family with four trahormone secretion, but does not produce a functional plasma membrane K+ current by itself. C;Genetics:
A;Gene: task-5
A;Map position: 20q12
C;Reywords: transmembrane protein
C;Reywords: transmembrane segment #status predicted <TMS1>
F;7.30/Domain: transmembrane segment #status predicted <TMS2>
F;129-155/Region: hydrophobic cytoplasmic linker #status predicted <TMS3>
F;120-240/Domain: transmembrane segment #status predicted <TMS3>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVIFKHIEGWSALDAIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWF---WILVGLA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 FCMLYALAGIPLGLIMFQSIGERMNTFAAKLL-----RFIRRAAGKQPIVTSSDLIIFCT 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              218 GC-VLFVALPAVIFKHIEGWSALDAIYFVVITLTTIGFGDYVA---GGS---DIEYLDFY 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable potassium channel chain n2P38 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T43509
R;Wang, Z.W.; Salkoff, L.
submitted to the EMBL Data Library, August 1998
A;Reference number: Z22450
A;Residues: 1-329 <WAN>
A;Residues: 1-329 <WAN>
A;Residues: 1-329 <WAN>
A;Residues: UNIPROT:017185; EMBL:AF083652; PIDN:AAG32863.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLFGFLLAGVGDQLGTIFGKGIAKVEDTF-IKWNVSQTKIRIISTIIFILFGCVLFVALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKRONIRTLSLIVCTLTYLLVGAAVFDALETENEILORKLVQRVREKLKTKYNMSNA-DY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCIIYALLGIPLFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110 --INAGIIPLGNSSNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42 MKWKTVSTIFLVV--VLYLIIGAAVFKALEQPQEISQRTTIVIOKQTFIAQHACVNSTEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DELIQQIVAAI -- NAGIIPLGNSSNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                    31;
                                                                                                                                                                                                                                                                                                                                                                                      Length 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 329;
                                                                                                                                                                                                                                                                                                                                                                                 Query Match 16.8%; Score 351.5; DB 2; Length Best Local Similarity 35.0%; Pred. No. 6.6e-21; Matches 91; Conservative 44; Mismatches 94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         284 YFAAVLSMI-----GDW 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 VIGAFLNLVVLRFLVASADW 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2
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50 IFLVVVLYLIIGAAVFKALEQPQEISQRTTIV---IQKQTFIAQHACVNSTELDELIQQI 106
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submitted to the EMBL Data Library, March 1996
A.Reference number: Z19188
A.Accession: T19860
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Rociocule type: DNA
A.Residues: 1-334 «WIL»
A.Cross-references: EMBL:Z70266; PIDN:CAA94204.1; GSPDB:GN00028; CESP:C40C9.1
A.Experimental source: clone C40C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  234 FILIGLAVFSACVNLL-------VLGFMASNADEVTA-----AQREPPSAIV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Map position: X
A;Introns: 34/1; 60/2; 98/1; 145/3; 160/3; 181/1; 204/1; 252/2; 279/2; 306/3
                                                                                                                                                                                                                                                                                                              Species: Caenorhabditis elegans
;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
;Accession: T19860
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C,Species: Caenorhabditis elegans
C,Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 VAAINAGIIPLGNSSNQVSH-WDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 FEAIAIKSIP----QQAGYQWQFAGAFYFATVVITTVGYGHSAPSTNAGKLFCMIFALF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219 CVLFVALPAVIFKHIEGWSALDAIYFVVITLTTIGFGDYV--AGGSDIEYLDFYKPVVWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WILVGLAYFAAVLSMIGDWLRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRLSVEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 LILSTFTYLLFGAMVFDKLE----SEKDTWVRDEIERITDRLKHK-YNFSERD---LHL
278 ILVGLAYF-----AAVLSMIGDWLRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 286.5; DB 2; Length 3; Pred. No. 1.3e-15; 58; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                      hypothetical protein C40C9.1 - Caenorhabditis elegans
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A,Status: preliminary: translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-364 «WAN>
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R; Wang, Z.W.; Salkoff, L.
submitted to the EMBL Data Library, August 1998
A; Description: Potassium channels in C. elegans.
A; Reference number: Z22450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 28.7%;
Matches 90; Conservative 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              337 YDKFQRATSVKRKL 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ::| | ::
274 LERFTRNSLVDSQI 287
                                                                                                   RLSV 334
                                                                                                                                                       349 YMGL 352
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                                                                                                      331
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C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C; Accession: T23182
R; Dobson, R.
submitted to the EMBL Data Library, June 1996
A; Reference number: 219703
A; Accession: T23182
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-383 «MIL»
A; Residues: 1-383 «MIL»
A; Residues: 1-383 «MIL»
A; Residues: CESP: KO1D12.4
A; Rapperimental source: clone KO1D12
C; Genetics:
A; Gene: CESP: KO1D12.4
A; Map position: 5
A; Introns: 28/3; 76/3; 184/2; 217/2; 270/2; 295/2
                                                      10,
                                                                                                                                                                                                                                        69 ISDYCDKPVTLPPTYDDTPYTWTFYHAFFFAFTVCSTVGYGNISPTTFAGRMIMIAYSVI 128
                                                                                                                                                                                                                                                                                                                                              182 ILRSLRERKIRYRLKESGNKPVTLLLINNEDFNESSSSCGGHMDNWRPSVYKVFFILFSMC 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 LVLITASAGIYSVVENWNYIDSLYFCFISFATIGFGDYVSNQQDVTRMSPDLYRFVNFCL 301
                                                                                                      50 IFLVVVLYLIIGAAVFKALEQPQE----ISQRTTIVIQKQTFIAQHACVNSTELDELIQQ 105
                                                                                                                                                                                                          106 IVAAINAGIIPLGNSSNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALL 165
                                                                                                                                                                                                                                                                                                                   GIPLFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVS-----QTKIRIISTIIFILF-G 218
                                                                                                                                                                                                                                                                                                                                                                                                                     219 CVLFVALPAVIFKHIEGWSALDAIYFVVITLTTIGFGDYVA------GGSDIEYLD 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                  269 FYKPVVWFWILVGLAYFAAVLSMIGDWLRVISKK----TKEEVGEFRAHAAEWTANVTAE 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75 SQRTTI----VIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNSSNQVSHWDLGS 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLG----IPLFGFLLAGVGDQLGTIFGK 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 SLFFSATVISTIGFGTSTPRTHLGRFITIVYGVVGCTCCVLFFNLFL----ERLVTGMSY 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   220 VLFVALPAVIFKHIEGWSALDAIYFVVITLTTIGFGDYVAGGSDIEYL--DFYKPVVWFW 277
                                                                                                                                       71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 NSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVVLYLIIGAAVFKALEQPQEI
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74;
                                                      36;
        Length 1001;
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Query Match 15.6%; Score 325; DB 2; Length 10
Best Local Similarity 28.8%; Pred. No. 3.5e-18;
Matches 90; Conservative 62; Mismatches 125; Indels
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299 VGYLRRMLN-ELY 310
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hypothetical protein Y39B6B.f [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 2.1-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C;Accession: T45032
R;Wilson, R.; Ainscough, R.; Anderson, K.; Baynes, C.; Berks, M.; Bonfield, J.; Burton, R; Wilson, L.; Gardner, A.; Green, P.; Hawkins, T.; Hillier, L.; Jier, M.; Johns B.; O'Callaghan, M.; Parsons, J.; Percy, C.; Rifken, L.; Roopra, A.; Saunders, D. Nature 368, 32-38, 1994
A;Authors: Shownkeen, R.; Sims, M.; Smaldon, N.; Smith, A.; Smith, M.; Sonnhammer, B.; & A;Authors: Shownkeen, R.; Wohldman, P.
A;Authors: Shownkeen, R.; Sims, M.; Smaldon, N.; Smith, A.; Smith, M.; Sonnhammer, B.; & A;Attle: 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.
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                                                                                                                                                                                                                      107 VAAINAGIIPLGNSSNQVSH-WDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALL 165
                                                                                                                                                                                                                                                                65 FEAIAIKSIP----QAAGYQWQFAGAFYFATVVITTVGYGHSAPSTNAGKLFCMIFALF 119
                                                                                                                                                                                                                                                                                                              GIPLFGFLLAGVGDQLGTIFGKGIAKVEDTFIK-----WNVSQTKIRIIS-TIIFILFG 218
                                                                                                                                                                                                                                                                                                                                                                                                   CVLFVALPAVIFKHIEGWSALDAIYFVVITLTTIGFGDYV--AGGSDIEYLDFYKPVVWF 276
                                                                                                                                                                                                                                                                                                                                                                                                                        277 WILVGLAYFAAVLSMIGDWLRVISKKTKEEVĢEFRAHAAEWTANVTAEFKETRRLSVEI 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96 STELDELIQQIVAAIN-----AGIIPLGNSSNQVS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --BRDELIRRTVYKINQLQIKRQRRLMTABBEYNRTAKVLTTFQETLGIVPA--DMDKDI 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HWDLGSSFFFRAGIVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQLGTIF 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans
Cipcussium channel chain n2P18 homolog - Caenorhabditis elegans
Cipcus: Caenorhabditis elegans
Cipcus: Caenorhabditis elegans
Cipcus: Caenorhabditis elegans
Cipcus: Canal-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
Cipcus: T43394
R;Kunkel, M.T.; Salkoff, L.
submitted to the EMBL Data Library, August 1998
A;Description: Potassium channels in C. elegans.
A;Reference number: Z22479
A;Reference number: Z22479
A;Reference number: Z22479
A;Reference number: Affile (FMBL)
A;Residues: 1-461 *KUN>
A;Residues: 1-461 *KUN>
A;Residues: 1-461 *KUN>
A;Cross-references: UNIPROT:Q18120; EMBL:AF083650; PIDN:AAC32861.1
                                                                                                                                                             10 TILTTFQKTFKGLLPLIILVAYTLLGAWIFWMIEGENE---REMLIEQQK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 129;
A; Cross-references: UNIPROT:076790; EMBL:AF083646; PIDN:AAC32857.1
                                           Length 364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 461;
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                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 13.4%; Score 279.5; DB 2; Best Local Similarity 23.5%; Pred. No. 6.8e-15; Matches 102; Conservative 70; Mismatches 133;
                                           DB 2;
                                       / Match 13.7%; Score 286.5; DB 2; Local Similarity 28.7%; Pred. No. 1.4e-15; les 90; Conservative 58; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :||:||| |:| :::
234 FILIGLAVFSACVNLL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 337 YDKFQRATSVKRKL 350
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274 LERFTRNSLVDSQI 287
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                                                              Best Loc
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A;Residues: 1-393 -WIL>
A;Cross-references: UNIPROT:Q9XU07; EMBL:Z92813; PIDN:CAB07286.1; GSPDB:GN00021; CESP:T2
A;Experimental source: clone T28A8
----PIVGVLLLIGLSLVSTVMTLIQQQIEALASGMKDNIDQEYARALNEAREDGEVDEH 336
                                                                                                             337 VDPEEDPENNKKSFDAV--ISRMNWSKRGLYYLLPDSOKKELAKOSEKKMGRKSIKIO-- 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 EMRESGIGQHVVEDLAVKYVDNVTRILFEARDTHCIGAKHLRPGGEDEDY--NWTYMTAL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134 FFAGTVITTIGFGNISPRIEGGKIFCIIYALLGIPLFGFLLAGVGD------QLGTIFG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KGIAKVEDTFIKWNVSQTK------IRIISTIIFILFGCVL-FVALPAVIFK 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       232 HIEGWSALDAIYEVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSM 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein T28A8.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T25392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 WKTYARIILAHVSLIVLSVVYVGFGAFLFYQLEQDNEVEVRARNIERFNIHKRQMIEHLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140 MWEGWDFFSGFFYFFTTWTTVGFGDIVPLKREYYILDL-----CYIIIGLSITTMCIDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 --KQTFIAQHACVNST--ELDELIQQIVAAINAGII-----PLGNSSNQVSHWDLGSSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44 WKTVSTIFL------VVVLYLIIGAAVFKALEQPQEISQRTTIVIQ--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.3%; Score 279; DB 2; Length 393; ilarity 27.5%; Pred. No. 6.2e-15; Conservative 51; Mismatches 106; Indels
                                                        321 VTAEFKETRRLSVEIYDKFQRATSVKRKLSAELAGNHNQELTP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Map position: 3
A,Introne: 73/1; 112/3; 179/2; 209/3; 287/2; 310/3; 364/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rilloyd, C.

Submitted to the EMBL Data Library, March 1997

Areference number: Z20027

Alaccesion: T25392

Alstatus: preliminary; translated from GB/EMBL/DDBJ

Alfolecule type: DNA
                                                                                                                                                                                                            -: :: | |:: |
-TDNDLLETLIREE 405
                                                                                                                                                                         375 TSEREVLPPLLKAE 388
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Best Local Similarity
....hes 83; Conserv?
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A; Reference number: S43531; MUID: 94150718; PMID: 7906398 A; Accession: T45032 A; Status: preliminary; translated from GB/EMBL/DDBJ	OY 158 FCIIYALLGIPLEGFLLAGVGD
A;Molecule type: DNA A;Mesidues: 1223 <wil.> A;Cross-references: EMBL:AL132896; NID:g6434440; PIDN:CAB60911.1; PID:g6434446 A;Experimental source: clone Y3986B</wil.>	Qy 189 IAKVBDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAVPKHIEGWS 237
C.;Genetion: 3 A.Map position: 3 A.Introns: 47/2; 82/2; 106/3; 151/1; 220/1; 260/3; 370/3 A.Note: Y39B6B.f	Qy 238 ALDAIYFVVITLTTIGEGDYVAGGSDIEXLDFYKEVVWFWILVGLAYFAAVLSMIGD- 294
Query Match Best Local Similarity 25.8%; Score 271; DB 2; Length 392; Best Local Similarity 25.8%; Pred. No. 2.7e-14; Matches 82; Conservative 65; Mismatches 109; Indels 62; Gaps 12;	Qy 295 322
QY 7 LDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVVLY 57	Qy 323 AEFKETRRISVEIYDKFQRATSVKRKLSAELAGNHNQELTPCRRTLS 370
QY 58 LIIGAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQI-VAAINAGI 114	Oy 371 VNHLTSEREVL 381 : : : : Db 431 NEHDSCQIEAI 441
Qy 115 IPLGNSSNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLL 174 : :	RESULT 13
Qy 175 AGVGDQLGTIFGKGIAKVEDTFIKMNVSQTKIRIISTIIFILFGC 219 1 : : : : : : :	hypotherical protein (24%). • - demondrations elegans C;Species: Caenorhabditis elegans C;Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999 C;Accession: T15584
QY 220 VLFV-ALPAVIFKHIE-GWSALDAIYFVVITLTTIGFGDYVAGGS-DIEYLDFYKDVWF 276	Rivatio, T. Submitted to the EMBL Data Library, November 1995 A.Description: The sequence of C. elegans cosmid C24A3. A.Reference number: Z18373
Qy 277 WILVGLAYFAAVLSMIGD 294 :::	A;Accession: Ti5584 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-35 <fav> A;Residues: 1-35 <fav> A;Cross-references: EMBL:U40424; NID:gl065542; PID:gl065543; PIDN:AAA81455.1; CESP:C24A</fav></fav>
RESULT 12 T24265	C;Genetics: A;Gene: CESP:C24A3.6 A;Introns: 21/1; 63/3; 131/1; 193/3; 206/3
Nypothetical protein Tolid Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C;Accession: T24265	Query Match 12.9%; Score 269; DB 2; Length 325; Best Local Similarity 25.4%; Pred. No. 3:2e-14; Matches 87; Conservative 53; Mismatches 87; Indels 116; Gaps 11;
R.Wilkinson, J. submitted to the EMBL Data Library, March 1996 A:Reference number: Z19866 A:Accession: T24265	Qy 46 TVSTIFLVVVLYLLIGAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVN 95
A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-52 VMIL> A;Crose-references: UNIPROT:022042; EMBL:Z70036; PIDN:CAA93875.1; GSPDB:GN00028; CESP:Td	QY 96 STELDELIQQIVAAINAGIIPLGNSSNQVS 125
A;Experimental source: clone T01B4 C;Genetics: A;Gene: CESP:T01B4.1 A;Map position: X	Qy 126 HWDLGSSFFFAGTVITTIGFGNISPRTBGGKIFCIIYALLGIPLFGFLLAGVGDQLGTIF 185
Query Match 12.9%; Score 270.5; DB 2; Length 522; Best Local Similarity 23.7%; Pred. No. 4.2e-14; Matches 102; Conservative 64; Mismatches 136; Indels 129; Gaps 15;	
Qy 50 IFLVVVLYLIIGAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTE 98	223 LSPPISGLLITVIWVIFCAVLFTFLEEWDFGTSLYFTLISFTTIGFGDILPSDYDFM
Oy 99 LDELIQQIVAAINAGIIPLGNSS-NQVSHWDLGSSFFRAGTVITTIGFGNISPRTEGGKI 157	Qy 268 DFYKPVWFWILVGLAYFAAVLSMIGDWLRVISKKTKE 305

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completed: July 13, 2005, 08:45:42
he : 23.6316 secs
    A;Experimental source: clone F19D8
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RESULT 14

H88124
protein T12C9.3 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: H88124
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genneme sequence of the nematode C. elegans: a platform for investigating biolog
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: H88124
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1910 c$STO>
A;Cross-references: GB:chr_II; PIDN:AC71141.1; PID:gl086770; GSPDB:GN00020; CESP:T12C9.3
A;Note: proline-rich
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Map position: 2
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Cipate: 15-Oct-1999 #text_change 09-Jul-2004
Cipate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
Cipate: 12118
Rishiburne, J.; Ainscough, R.
Rishiburne, J.
Ri
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEQPQE----ISQRITIVIQKQIFIAQHACVNSTELD------ELI------Q 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QIVAAINAGIIPL------GNSSNQVSH------WDLGSSFFFAG 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             279 QYVRYSDVRTIGFEGRSSYEEADETGGDSERKRRHRHGNKRGDRGSEKWMTTSSALFFAA 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138 TVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQLG--TIF-----GKGIA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              221 LEVALPAVIERGHIEGWSALDAIYEVVITLITIGEGDYVAGGSDIEYLDFYKPVVWFWILV 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162 PQFSRRFSIFPGLLESARPDDETTTTLQNIRKYAKLALPHIVLVVCVCIYATIGAWIFYT 221
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLAYFAAVLSMIG--------DWLRVISKKTK-------EEVGEFRAH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           206 SKRELKKQSDEHLLREIAEVSPYLDVLLVAGLFVVFIAIGSAVIPLWENQLTYFDSVYFS 265
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A;Map position: X
A;Introns: 31/1; 82/2; 101/3; 157/1; 197/1; 230/3; 267/2; 325/3; 356/1; 404/3
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                                                                                                                                                                                                                                                    26 KLKCNSKCAMMKFRNVLRIALGHLALYCFVVCYVFAGAWVFHQLEGENETELHDKQREYA
                                                                                                                                                                                                                                                                                                                                                 32 RVESDSAINVMKWKTVSTI-----FLVVVLYLLIGAAVFKALEQPQEI----SQRTTI
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                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32;
                                                                                                                 Query Match
12.6%; Score 263; DB 2; Length 452;
Best Local Similarity 29.3%; Pred. No. 1.4e-13;
Matches 86; Conservative 52; Mismatches 124; Indels
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Sequence 60, Appl Sequence 89, Appl Sequence 8, Appli Sequence 8, Appli Sequence 7, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 66, Appli Sequence 2, Appli Sequence 2, Appli

Sequence 57, Sequence 58,

Sequence 73, Appli Sequence 106, Appli Sequence 2, Appli Sequence 10, Appl Sequence 55, Appl Sequence 55, Appli Sequence 2, Appli Sequence 2, Appli Sequence 44, Appli Sequence 44, Appli

Sequence 64, App Sequence 29, Appl

Sequence 65,

Sequence 29,

Sequence Sequence Sequence

Sequence 8, 7 Sequence 19, Sequence 12,

us-09-503-089a-4.rapb

Title: Perfect score:

Sequence:

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OM protein

Run on:

Scoring table:

Searched:

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Minimum I Maximum I

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1 MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVVLYLII
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US-09-828-035-2
US-10-343-035-2
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FRIENT NO. US20020028485A1
GENERAL INFORMATION:
FRAPLICANT: Helen Jane Meadows
APPLICANT: Helen Jane Meadows
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30031-D1
CURRENT APPLICATION NUMBER: US/09/828,746
CURRENT APPLICATION NUMBER: US 09/236,080
FRIOR APPLICATION NUMBER: US 09/236,080
FRIOR FILING DATE: 1999-01-25
RIOR FILING DATE: 1998-01-27
FRIOR FILING DATE: 1998-00-9
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 6
LENGTHA: 411
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Sequence 2, Appli
                                                                                                                                                         July 13, 2005, 08:40:02; Search time 90.2442 Seconds (without alignments) 1759.475 Million cell updates/sec
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Sequence 2, Ag
Sequence 31, 7
Sequence 83, 7
Sequence 18, 7
Sequence 18, 7
Sequence 20, 7
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                      GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-870-492-45
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US-09-828-746-2
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Listing first 45 summaries
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61 GAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS 120

1 MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVVLYLII

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Sequence 45,

Sequence 45,

20044 200444 200444 200444 20033 200411

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Result

9

Gaps

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Length 411; 1; Indels

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RESULT 3
US-10-121-746-83
US-10-121-746-83
Sequence 83, Application US/10121746
Publication No. US20030036648A1
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 96.4%
Matches 396; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT; ORGANISM: H. sapiens
US-10-121-746-83
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                                                                                                                                             241 AIXFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS 300
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                                                                                                KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSAELAGNHNQ
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                                                                                                                                                                                                                                                                                                           US-09-828746-5

SQUENCE 2, Application US/09828746

Patent No. US20020028485A1

GENERAL INFORMATION

APPLICANT: Helen Jane Meadows

APPLICANT: CORRAG Gerald Chapman

TITLE OF INVENTION: NOVEL COMPOUNDS

FILE REFERENCE: GP-30031-D1

CURRENT APPLICATION NUMBER: US/09/828,746

CURRENT FILING DATE: 1999-01-25

PRIOR FILING DATE: 1999-01-25

PRIOR FILING DATE: 1998-01-27

PRIOR FILING DATE: 1998-01-27

PRIOR FILING DATE: 1998-00-9

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FASELSEQ for Windows Version 3.0

SEQ ID NO 2

LENGTH: 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
CRGANISM: HOMO SAPIENS
US-09-828-746-2
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SNQVSHWDLGSSFFRAGTVITTIGFGNISPRTEGGRIFCIIYALLGIPLFGFLLAGVGDQ 180 120 61 GATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQIVAAINAGIIPLGNT 120 300 KKTKEEVGEFRAHAAEWTANVTAEFKETRRLSVEIYDKFORATSVKRKLSAELAGNHNO 360 GAAVFKALEQPOEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS 1 MAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVVLYLII 1 MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVVLYLII APPLICANT: Miller, Andrew P.
APPLICANT: Curran, Mark Edward
APPLICANT: Hiller, Andrew P.
APPLICANT: Willer, Andrew P.
APPLICANT: Will Ping
APPLICANT: Warc
APPLICANT: Wang, Jian-Wang
APPLICANT: Wang, Jian-Wang
APPLICANT: Wang, Jian-Wang
TITLE OF INVENTION: No. US20030036648Alel Human Potassium Channels
FILE REFERENCE: SEQ-15P
CURRENT APPLICATION NUMBER: US/09/336,643A
FRIOR PAPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/076,687
FRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/116,448
FRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-01-19
FRIOR FILING DATE: EARLIER FILING DATE: 1999-01-19
FRIOR FILING DATE: EARLIER FILING DATE: 1999-01-19
FRIOR FILING DATE: EARLIER FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 87
SOFTWARE: FASTSEQ for Windows Version 4.0 Gaps PCT/US99/03826 ö Length 411; ELTPCRRTLSVNHLTSEREVLPPLLKAESIYLNGLTPHCAGEDIAVIENMK Indels 97.8%; Score 2044; DB 14; 96.4%; Pred. No. 3.5e-185; attive 11; Mismatches 4;

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61 GAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS 120
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; Sequence 83, Application US/10976644
; Publication No. US20050112662A1
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Willer, Marc
; APPLICANT: Wang, Jian-Wang
TITLE OF INVENTION: Novel Human Potassium Channels
; TILE REFERENCE: SEQ-15P
CURRENT APPLICATION NUMBER: US/10/976,644
; CURRENT APPLICATION NUMBER: US/09/336,643
; PRIOR PELICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1999-06-18
; PRIOR FILING DATE: 1999-01-19
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ 1D NOS: 87
                                    Score 2044; DB 16;
Pred. No. 3.5e-185;
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96.4%; Pred. No. 3.5e-185;
tive 11; Mismatches 4;
                                                                             11; Mismatches
                                  97.8%;
                                                                             Matches 396; Conservative
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Best Local Similarity 96.4
Matches 396; Conservative
                                    Query Match
Best Local Similarity
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US-10-976-644-83
US-10-349-528-31
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Sequence 31. Application VS/10349528

Publication No. US2004025366811

GENERAL INFORMATION:
APPLICANT: RAMANATHAN, Chandra
APPLICANT: FEDER, John
TITLE OF INVENTION: USE THEREOF
TITLE OF INVENTION: USE THEREOF
TITLE OF INVENTION: USE THEREOF
TITLE OF INVENTION: USE 10210
CURRENT FILING DATE: 2003-01-22
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn version 3.2
SEQ ID NO 31
LENGTH: 411
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        | Sequence 2, Application US/10745210
| Publication No. US20040143855A1
| GENERAL INFORMATION: US20040143855A1
| APPLICANT: TONONY, Giulio
| APPLICANT: CIRELLI, Chiara
| TITLE OF INVENTION: ION CHANNELS AS TARGETS FOR SLEEP-RELATED DRUGS
| FILE REFERENCE: 054030-0044
| CURRENT APPLICATION NUMBER: US/10/745,210
| CURRENT PILING DATE: 2003-12-23
| PRIOR PILING DATE: 2001-12-23
| NUMBER OF SEQ ID NOS: 2
| SOFTWARE: Patentin version 3.2
| SEQ ID NO 2
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96.4%; Pred. No. 3.5e-185;
iive 11; Mismatches 4;
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ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
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LGTIFGKGIAKVEDTFIKMNVSQTKIRIISTIIFILFGCVLFVALPAVIFKHIEGWSALD 240
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LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAIIFKHIEGWSALD 240
                                        AIYFVVITITTIGFGDYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS 300
                                                                                                                   KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSAELAGNHNQ 360
                                                                                                                                         SNOVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180
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APPLICANT: LESAGE, FLORIAN
APPLICANT: LESAGE, FLORIAN
APPLICANT: ROMEY, GEORGES
TITLE OF INVENTION: HUAN TAREZ, A STRETCH-AND ARACHIDONIC ACID-SENSITIVE
TITLE OF INVENTION: HUAN TAREZ, A STRETCH-AND ARACHIDONIC ACID-SENSITIVE
TITLE OF INVENTION: RILUZOLE
FILE REFERENCE: 1256-R-00
CURRENT APPLICATION NUMBER: US/09/892,360
CURRENT FILING DATE: 2001-06-27
RIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 18
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; Pred. No. 6.7e-185;
12; Mismatches 4;
                                                                                                                                                                                                                                                                                                                             Sequence 18, Application US/09892360; Publication No. US20040101833A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 96.1%;
Matches 395; Conservative 12
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; ORGANISM: Mus
US-09-892-360-18
                                                                                                                                                                                                                                                                                                                   US-09-892-360-18
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Publication No. US20050112663A1

GENERAL INFORMATION:

APPLICANT: Miller, Andrew P.

APPLICANT: Curran, Mark Edward

APPLICANT: Hu, Ping

APPLICANT: Rutter, Marc

APPLICANT: Novel Human Potassium Channels

TITLE OF INVENTION: Novel Human Potassium Channels

TITLE OF INVENTION: Novel Human Potassium Channels

FILE REFERENCE: SEQ-15P

CURRENT PILING DATE: 2004-10-29

PRIOR PELICATION NUMBER: G0/076,687

PRIOR PELICATION NUMBER: 60/076,687

PRIOR PELING DATE: 1999-01-07

PRIOR PELING DATE: 1999-01-19

PRIOR PELING DATE: 1999-01-19
                                                                                                                                                                                                                                                          241 AIYEVVITLITIGFGDYVAGGSDIEYLDFYKPVWFWILVGLAYFAAVLSMIGDWLRVIS
                        SNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ
                                                                                                                                                                                  LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAIIFKHIEGWSALD
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                                                                              SNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ
                                                                                                                                                           LGTI FGKGIAKVEDTFI KWNVSQTKIRI I STI I FILFGCVL FVALPAVI FKHI EGWSALD
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96.4%; Pred. No. 3.5e-185;
live 11; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 96.4<sup>†</sup>
Matches 396; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 411
; TYPE: PRT
; ORGANISM: H. sapiens
US-10-976-647-83
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136 SNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 96.2%; Score 2011; DB 8; Length 4 Best Local Similarity 95.1%; Pred. No. 5e-182; Matches 391; Conservative 13; Mismatches 7; Indels
                                      SOFTWARE Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,011
FILING DATE: 11-MAR-1997
CLASSIFICATION: 536
ATTONREY/AGENT INPOMMATION:
NAME: Matthews, Gale F.
REGISTRATION NUMBER: 32,269
REFERENCE/DOCKET UNBER: 32,421-C2
TELECOMMULICATION INFORMATION:
TELEPHONE: 201-683-2134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 45, Application US/10870492

Sequence 45, Application US/10870492

Publication No. US20050032165A1

GENERAL INFORMATION:

APPLICANT: PAUSCH, NAKE H.

TITLE OF INVENTION: AND METHODS OF USING SAME

FILE REFERENCE: 01142.0114 SEQUENCE LISTING

CURRENT APPLICATION NUMBER: US/10/870,492

CURRENT FILING DATE: 2004-06-18

PRIOR APPLICATION NUMBER: US/09/503,849

PRIOR APPLICATION NUMBER: 08/816,011

PRIOR FILING DATE: 1997-03-11

PRIOR FILING DATE: 1997-03-11

PRIOR FILING DATE: 1995-10-25

PRIOR FILING DATE: 1995-10-25
                                                                                                                                                                                                                                                                                                                      TELEFAX: 201-683-4117
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 426 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
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US-10-870-492-45
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  Sequence 20, Application US/10349528
Publication No. US20040253668A1
GENERAL INFORMATION:
APPLICANT: RAWANATHAN, Chandra
APPLICANT: GOPAL, Shuba
APPLICANT: FEDER, John
TITLE OF INVENTION: USE THEREOF
FILE REFERENCE: DOING
CURRENT PILING DATE: US/10/349,528
CURRENT FILING DATE: 2003-01-22
NUMBER OF SEQ ID NOS: 35
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Sequence 45, Application US/08816011
Publication No. US20030165806A1
GENERAL INFORMATION:
APPLICANT: Price, Laura A.
APPLICANT: Prace, Laura A.
TITLE OF INVENTION: Potassium Channels, Nucleotide Sequences
TITLE OF INVENTION: Botassium Channels, Nucleotide Sequences
TITLE OF EQUENCES: 56
CORRESPONDENCES 56
CORRESPONDENCE ADDRESS:
ADDRESSEB: American Home Products Corporation
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: USA
ZIP: O7054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELTPCRRTLSVMHLTSERDVLPPLLKTESIYLNGLTPHCAGEBIAVIENIK 422
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                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin version 3.2
SEQ ID NO 20
LENGTH: 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 95.9
Matches 394; Conservative
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US-10-349-528-20
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US-08-816-011-45
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TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM, TITLE OF INVENTION: AND METHODS OF USING SAME
FILE REPERENCE: 0.1142.0.114. SEQUENCE LISTING
CURRENT APPLICATION NUMBER: US/10/870,492
CURRENT PILING DATE: 2004-06-18
PRIOR FILING DATE: 2000-02-15
PRIOR PELICATION NUMBER: US/09/503,849
PRIOR PELICATION NUMBER: 08/816,011
PRIOR APPLICATION NUMBER: PCT/US95/14364
PRIOR FILING DATE: 1995-03-11
PRIOR PELICATION NUMBER: PCT/US95/14364
PRIOR FILING DATE: 1995-10-25
PRIOR FILING DATE: 1995-10-31
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                           16 VAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVVLYLII
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    MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVVLYLII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 58, Application US/10870492; Publication No. US20050032165A1; GENERAL INFORMATION:
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SEQ ID NO 58
LENGTH: 426
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US-10-870-492-58
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US-10-870-492-57
Sequence 57, Application US/10870492
Sequence 57, Application US/10870492
Sequence 57, Application Word US20050032165A1
GENERAL INFORMATION:
THE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES
TITLE OF INVENTION: AND METHODS OF USING SAME
TITLE OF INVENTION: AND METHODS OF USING SAME
STILE OF INVENTION: AND METHODS OF USING SAME
CURRENT APPLICATION NUMBER: US/10/870,492
CURRENT APPLICATION NUMBER: US/09/503,849
PRIOR FILING DATE: 2000-02-16
PRIOR PELING DATE: 1997-03-11
PRIOR PELING DATE: 1997-03-11
PRIOR PELING DATE: 1997-03-11
PRIOR PELING DATE: 1997-03-11
SPRIOR PELING DATE: 1997-03-11
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PATENTIN VORE: 07/332,312
SEQ ID NO S7
TEMPORAL SECOND NOS: 74
SEQ ID NO S7
TEMPORAL SECOND NO S7
TEMPORAL SECOND NO S7
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95.1%; Pred. No. 5e-182;
tive 13; Mismatches 7;
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PRIOR FILING DATE: 1994-10-31
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 45
LENGTH: 426
                                                                                                                                                                                Query Match
Best Local Similarity 95.1<sup>5</sup>
Matches 391, Conservative
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CORGANISM: Homo sapiens
US-10-870-492-57
                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                              US-10-870-492-45
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Job time : 91.2442 secs
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; ORGANISM: Homo sapiens
US-10-870-492-59
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| Sequence 60. Application US/10870492
| Publication No. US20050032165A1
| CENERAL INFORMATION:
| APPLICANT: PAUSCH, MARK H. |
| TITLE OF INVENTION: AND METHODS OF USING SAME |
| TITLE OF INVENTION: AND METHODS OF USING SAME |
| TITLE OF INVENTION: AND METHODS OF USING SAME |
| FILE REFERENCE: 01142.0114 SEQUENCE LISTING |
| CURRENT PELIATION NUMBER: US/09/503, 849 |
| PRIOR PILING DATE: 2004-06-18 |
| PRIOR PELICATION NUMBER: 08/816,011 |
| PRIOR PILING DATE: 1997-03-11 |
| PRIOR PILING DATE: 1997-03-11 |
| PRIOR PILING DATE: 1997-10-31 |
| PRIOR PILING DATE: 1994-10-31 |
| PRIOR FILING DATE: 1994-10-31 |
| SEQ ID NO 60 |
| LENGTH's 426 |
| TENGTH'S 426 |

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301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSAELAGNHNQ 360
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US-10-870-492-60
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RESULT 15

US-10-870-492-59

i Bequence 59, Application US/10870492

i Publication No. US2055032165A1.

i GENERAL INFORMATION:

APPLICATION POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,

ITILE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,

ITILE OF INVENTION: AND METHODS OF USING SAME

ITILE OF INVENTION: AND METHODS OF USING SAME

CURRENT APPLICATION NUMBER: US/10/870,492

CURRENT FILING DATE: 2004-06-18

PRIOR FILING DATE: 1097-03-11

PRIOR FILING DATE: 1997-03-11

PRIOR FILING DATE: 1997-10-3-11

PRIOR FILING DATE: 1997-10-3-11

PRIOR FILING DATE: 1997-10-3-1

NUMBER OF SEQ ID NOS: 74
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July 13, 2005, 08:10:49; Search time 26.3635 Seconds (without alignments) 1163.760 Million cell updates/sec Run on:

US-09-503-089A-4 2090 1 MAAPDLLDPKSAAQNSKPRL...........LNGLTPHCAGEDIAVIENMK 411 score: Title: Perfect sc Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

513545 segs, 74649064 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

/cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:* Issued Patents AA: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 6, Appli		Sequence 83, Appl		700	73	7	Sequence 4, Appli	69	780	4,	7	7	14,	, S	'n	'n	Sequence 2, Appli	•	763	ν,	8,	8	80	12,	7	99
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SUMMARIES	αı	US-09-236-080-6	US-09-236-080-2	US-09-336-643A-83	US-09-144-914-8	US-09-949-016-7001	US-09-949-016-7368	US-09-432-470-2	US-09-432-470-4	US-09-949-016-6913	US-09-949-016-7809	US-09-236-080-4	US-09-561-763-2	US-09-431-367B-2	US-09-362-842-14	US-09-561-763-5	US-09-431-367B-5	US-08-749-816-2	US-09-144-914-2	US-09-144-914-4	US-09-949-016-7631	US-09-144-914-5	US-09-336-643A-81	US-09-561-763-8	US-09-431-367B-8	US-09-362-842-12	US-08-332-312-2	US-09-949-016-6654
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US-09-949-016-7794 US-09-362-842-6 US-08-332-312-4 US-09-362-842-4 US-09-362-842-4 US-09-270-767-45442 US-09-270-767-45442 US-09-270-767-45442 US-09-361-78-11 US-09-361-78-11 US-09-362-842-8 US-09-362-842-8 US-09-362-842-8 US-09-362-842-8 US-09-362-842-8 US-09-362-842-8 US-09-362-842-8 US-09-362-842-8	US-09-270-767-31685 US-09-614-480-2
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ALIGNMENTS

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61 GAAVFKALEQPQEISQRITIVIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS 120
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99.8%; Pred. No. 1.9e-210;
iive 0; Mismatches 1;
                                                                                                                                   Compounds
                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/236,080 CURRENT FILING DATE: 1999-01-25 NUMBER OF SEQ ID NOS: 6 SOFTWARE: FastSEQ for Windows Version 3.0
                                 Sequence 6, Application US/09236080
Patent No. 6242217
GENERAL INFORMATION:
APPLICANT: Helen Meadows
APPLICANT: Conrad Chapman
TITLE OF INVENTION: No. 6242217el C
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 99.8
Matches 410; Conservative
                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Mus musculus
RESULT 1
US-09-236-080-6
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Gaps

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KKTKBEVGEFRAHAAEWTANVTAEFKETRRLSVEIYDKFORATSVKRKLSAELAGNHNO

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APPLICANT: Rutter, Marc
TITLE OF INVENTION: No. 6399761el Human Potassium Channels
TITLE OF INVENTION: NO. 6399761el Human Potassium Channels
CURRENT APPLICATION NUMBER: US/09/336,643A
CURRENT APPLICATION NUMBER: 60/076,687
PRIOR FILING DATE: 1999-06-18
PRIOR FILING DATE: 1999-01-19
PRIOR FILING DATE: 1999-01-19
PRIOR APPLICATION NUMBER: 60/116,448
                                                                     APPLICANT: Helen Meadows
APPLICANT: Conrad Chapman
TITLE OF INVENTION: NO. 6242217el Compounds
FILE REFERENCE: GP30031
CURRENT APPLICATION NUMBER: US/09/236,080
CURRENT FILING DATE: 1999-01-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 83, Application US/09336643A Patent No. 6399761 GENERAL INFORMATION: APPLICANT: Miller, Andrew P. APPLICANT: Curran, Mark Edward
                Sequence 2, Application US/09236080 Patent No. 6242217 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                          TYPE: PRT
CORGANISM: Homo sapiens
US-09-236-080-2
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US-09-236-080-2
                                                                                                                                                                                                                                                        LENGTH: 411
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APPLICANT: Duprat, Fabrice

APPLICANT: Leasge, Florian
APPLICANT: Leasge, Florian
APPLICANT: Leasge, Florian
APPLICANT: Leasge, Michel
APPLICANT: Lazdunski, Michel
APPLICANT: Lazdunski, Michel
TITLE OF INVENTION: PAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
FILE REFERENCE: 989.6705CHP
CURRENT APPLICATION NUMBER: U8/09/144,914
CURRENT FILING DATE: 1998-09-01
EARLIER PILING DATE: 1998-09-01
EARLIER FILING DATE: 1998-08-04
EARLIER FILING DATE: 1998-08-04
EARLIER FILING DATE: 1998-08-04
EARLIER FILING DATE: 1996-02-08
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATCHIN VOIC: 2.0
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                                                                                                                                                            97.8%; Score 2044; DB 3; Length 411;
llarity 96.4%; Pred. No. 3e-206;
Conservative 11; Mismatches 4; Indels (
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PRIOR FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PSECSEQ for Windows Version 4.0
SEQ ID NO 83
LENGTH: 411
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Patent No. 6309855
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US-09-144-914-8
                                                                                                               sapiens
                                                                                                                                                                Query Match
Best Local Similarity
Matches 396; Conserv
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                                                                                                                   ; OKGANISM: n. ;
US-09-336-643A-83
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                                                                                                           ORGANISM: H.
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                                                                                            TYPE: PRT
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JAPLICATI: VENTEAL INFORMATION: DELYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TILE REPERENCE: CLOOO.-04-14
CURRENT APPLICATION NUMBER: 60/231,768
PRIOR PELING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PLING DATE: 2000-010-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                               216 GFLLAGIGDQLGTIFGKSIARVEKVÇRKKQVSQTKIRVISTILFILAGCIVFVTIPAVIF 275
                                                                            KHIEGWSALDAIYFVVITLTTIGFGDYVAGG-SDIEYLDFYKPVVWFWILVGLAYFAAVL 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 FLVVVLYLIIGAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAI 110
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     GFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAVIF 230
                                                                                              NAGIIPLGNSSNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLF
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                                                                                                                                                                                                                          - KRKLSAELAGNHNQELTPCRRTL 369
                                                                                                                                                                                                                                              :|:| : |:| 376 ERRLGLDQRAHSLDMLSPEKRSV 399
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Matches 247; Conservative
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
FRIOR APPLICATION NUMBER: 60/231,768
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRESE FRESEQ for Windows Version 4.0
SEQ ID NO 7001
LENGTH: 538
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                                                       1 MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVVLYLII
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S9.9%; Score 1251.5; DB 4;
Best Local Similarity 64.3%; Pred. No. 1.1e-122;
Matches 247; Conservative 54; Mismatches 66;
   2e-186;
 Pred. No. 2e-1
; Mismatches
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US-09-949-016-7001
; Sequence 7001, Application US/09949016
; Patent No. 6812239
al Similarity 99.5%;
366; Conservative
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 Local Similarity
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US-09-949-016-7001
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Query Match
38.1%; Score 797; DB 4; Length 393;
Best Local Similarity 51.1%; Pred. No. 4.5e-75;
Matches 145; Conservative 60; Mismatches 77; Indels
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        77; Indels
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Patent No. 6426197
GENERAL INFORMATION:
APPLICANT: David Malcolm Duckworth
APPLICANT: Conrad Gerald Chapman
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REPERENCE: GP-30190
CURRENT FILING DATE: 1999-11-03
EARLIER FILING DATE: 1999-11-03
EARLIER FILING DATE: 1999-11-03
EARLIER FILING DATE: 1999-11-03
SARLIER FILING DATE: 1999-11-03
SARLIER FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Fast-SEQ for Windows Version 3.0
SERIOTON
                                                               Sequence 2, Application US/09432470
| Patent No. 6426197
| GENERAL INFORMATION:
| APPLICANT: David Malcolm Duckworth
| APPLICANT: David Malcolm Duckworth
| TITLE OF INVENTION: NOVEL COMPOUNDS
| TILE REFERENCE: GP-30190
| CURRENT FILING DATE: 1999-11-03
| FARLIER APPLICATION NUMBER: UK 9923668.9
| EARLIER APPLICATION NUMBER: UK 9824048.4
| SARLIER FILING DATE: 1999-10-07
| SARLIER FILING DATE: 1999-11-03
| NUMBER OF SEQ ID NOS: 4
| SOFTWARE: FastSEQ for Windows Version 3.0
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CORGANISM: HOMO SAPIENS
US-09-432-470-4
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOOI307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-30
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-0-0-08
RIGHT APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-0-0-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
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Mismatches

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Matches 107; Conservative
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US-09-431-367B-2
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                                                                                     ABELICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949, 016
CURRENT PILING DATE: 2000-04-14
RRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FREESEQ for Windows Version 4.0
LENGTH: 440
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51.1%; Pred. No. 5.3e-75;
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                                                          Sequence 7809, Application US/09949016
Patent No. 6812339
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Matches 145; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Human
                                              US-09-949-016-7809
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US-09-236-080-4
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LENGTH: 107
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26.4%; Score 551; DB 3; Length 107; 100.0%; Pred. No. 4.7e-50;

Query Match Best Local Similarity

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NSSNQVSHWDLGSSFFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVG 178
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                                                                                         1 NSSNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Curtis, Rory A.J. et al.
TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR CURRENT APPLICATION NUMBER: US/09/561,763
CURRENT FILING DATE: 2000-04-29
PRIOR PILING DATE: 01-11-1999
PRIOR PILING DATE: 01-11-1999
PRIOR PILING DATE: 01-03-1999
NUMBER OF SEO ID NOS: 12
SOFTWARE: PATENTIN Ver. 2.0
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Patent No. 6670149

GENERAL INFORMATION:
APPLICANT: Curtis, Rory A.J.
TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
FILE REFERENCE: MNI-074CP
CURRENT PAPLICANION NUMBER: US/09/431,367B
CURRENT PILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: 09/259,951
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30.8%; Pred. No. 3e-35;
.ive 62; Mismatches 120; Indels
0; Indels
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Best Local Similarity 30.8%
Matches 105; Conservative
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CORGANISM: Homo sapiens
US-09-561-763-2
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RESULT 15
US-09-561-763-5
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                                                                                                                                                                                                                                                                             | : || || : : || || || 127 LTWI-SALGKFFGGRAKRLGQFLTKRGVSLRKAQITCTVIFIVWGVLVHLVIPPFVFMVT 185
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                                                                                                                                                                                                                                                             114 IIPLGNSSNOVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFL 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----RKESF 267
                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Buchman et al.
TITLE OF INVERTION: UNCLEIC ACIDS AND POLYPEPTIDES OF INVERTEBRATE TWIK
TITLE OF INVENTION: CHANNELS AND METHODS OF USE
FILE REPERENCE: 7326-104
CURRENT FILING DATE: 1999-07-28
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
LENGTH: 361
                                                                                                                                                                       Gaps
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                                                                                                                                      20.1%; Score 420; DB 4; Length 499; 30.8%; Pred. No. 3e-35; tive 62; Mismatches 120; Indels
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US-09-362-842-14
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Patent No. 6511824
PRIOR FILING DATE: 1999-03-01
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
                                                                                                                                                     Best Local Similarity 30.8
Matches 105; Conservative
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                                                                            TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 89; Conserva
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US-09-362-842-14
                                                                                              ; ORGANISM: HOT
US-09-431-367B-2
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                                                                                                                                       Query Match
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                                                                                        50 IFLWWINILIGAAVFKALEQPQEISQRTTIVIQKQTFIAQHACWNSTELDELIQQIVAA 109
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174 ALVERLLIPTVW------LLQWLNSKLGHLYQPLRIRIVHLAIIVLVLLVFFLLLP 223
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TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR TITLE REFRENCE: MNI-074CP2
CURRENT APPLICATION NUMBER: US/09/561,763
CURRENT PILING DATE: 2000-04-29
FRIOR APPLICATION NUMBER: 09/431,367
PRIOR FILING DATE: 01-11-1999
PRIOR FILING DATE: 01-03-1999
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 5
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Job time: 27.3635 secs
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284 MMLTLTVFYD 293
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ORGANISM: Homo sapiens
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Aab50046 F
Ady6698 F
Ady6698 P
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Compugen Ltd.
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GenCore version
Copyright (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
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AAU07625
AAU07624
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AAU79472
ABB83542
ADA05746
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Gapop 10.0 , Gapext 0.5
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26 1243 59.2 543 7 ADE08315 28 1239 59.2 543 8 ADN62910 29 1215.5 57.9 724 5 AAU14193 30 988 47.0 228 8 ADJ27190 31 803 38.2 39.3 AAV94426 33 803 38.2 39.3 AAV94426 34 803 38.2 39.3 AAV94426 35 803 38.2 39.3 AAV94426 36 803 38.2 419 7 AAE38597 37 803 38.2 419 7 AAE38597 38 803 38.2 419 7 AAE38597 40 803 38.2 419 8 ADH51639 38 803 38.2 419 8 ADH51639 38 803 38.2 419 8 ADH51639 40 803 38.2 419 8 ADH64894 41 803 38.2 419 8 ADH64894 42 803 38.2 419 8 ADH64894 43 776.5 37.0 398 2 AAY30647 44 768.5 36.6 398 5 AAE16598 45 636 3 38.2 419 8 ADR44894	Novel Human	Aau/94/3 human nov Aao14193 Human tra	Adj27190 Human TRI Abu60891 Human G p	Aay94426 Human h-T Aay94425 Human h-T	Aag67777 Human mec	Aag78406 Amino aci	Aae38597 Human pot	Hemato	Adh51639 Human 123	_	Adr44894 Polypepti	Aau04571 Human G-p	Abu60872 Human G p	Aay30647 A mechani	Aae16598 Human TWI	Abg02731 Novel hum
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ALIGNMENTS

Novel nucleic acid encoding a TREK-1 potassium channel protein for transfecting cells to be used to identify compounds with anesthetic Human; potassium channel protein; TREK-1; anaesthetic; analgesia; Ę, Patel ΰ Romey Human TREK-1 potassium channel protein. AAE10341 standard; protein; 411 AA Lesage F, Claim 3; Page 28; 39pp; English. (CNRS) CNRS CENT NAT RECH SCI 12-FEB-1999; 99US-0119727P. 11-FEB-2000; 2000WO-IB000226 (first entry) Honore WPI; 2000-549146/50. N-PSDB; AAD17496 WO200047738-A2 Homo sapiens Lazdunski M, 10-DEC-2001 17-AUG-2000. properties.

The invention relates to human and mouse TREK-1 potassium channel proteins and their corresponding DNA molecules. TREK-1 nucleic acid is useful for transfecting cells to induce expression of the TREK-1 potassium channel protein. These cells are then used in assays to identify compounds which have anaesthetic properties, producing a safe, reversible state of unconsciousness with concurrent amnesia and analgesia in a mammal upon inhalation. The present sequence is human TREK-1

Sequence 411 AA

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cc may be alpha subunits, which form the functional channel, or accessory subunits that act to modulate the channel activity. K+Hnov59 is a 4 transmembrane domain, 2 pore domain potassium channel. The gene is clocated on chromosome 19, determined via PCR chromosomal localisation clocated on chromosome 19, determined via PCR chromosomal localisation catesian of expressed sequence tags (ESTS) which were related but not identical to known human potassium channels. Potential polymorphisms detected as sequence variants between multiple independent clones. Conchemical pathways. Defective potassium channels are known to cause four human diseases: episodic ataxia with myokymis, cardiac arrhythmia clong QT syndrome); epilepsy; and Bartter's syndrome. As potassium channels are critical components of virtually all cells, it is likely that abnormal potassium channels are also implicated in certain renal, cardiovascular and central nervous system (CNS) disorders. Nucleotides encoding K+Hnov proteins may be used for identifying homologous or crelated proteins and the DNA sequences encoding them. They may be used to produce compositions that modulate the expression and function of the K+Hnov protein and in studying the biochemical pathways associated with it. They may also be used for the recombinant production of K+Hnov protein in fermentation cultures. Additionally, such nucleotides may be used in gene therapy protocols for the treatment of diseases associated with abnormal potassium channels.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acids encoding mammalian K+Hnov potassium channel proteins, useful for the diagnosis and treatment of episodic ataxia with myokymia, cardiac arrhythmia, epilepsy and Bartter's syndrome.
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                                                                                                                                                                                                                                                           LGTI FGKGIAKVEDTFI KWNVSQTKI RIISTII FILFGCVLFVALPAII FKHI EGWSALD
                                                                                                                                                                                                                                                                           LGTIFGKGIAKVEDTFIKMNVSQTKIRIISTIIFILFGCVLFVALPAIIFKHIEGWSALD
                                                                                                                                  GATVFKALEQPHE1SQRTT1V1QKQTF1SQHSCVNSTELDEL1QQ1VAA1NAG11PLGNT
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                                                                                       1 MAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVVLYLII
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                                                                     1 MAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVVLYLII
                                         Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome;
cardiovascular disorder; CNS disorder; renal disorder.
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           Length 411;
                                      Indels
                        8.8e-210;
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           DB 3;
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        i; Score 2100; Di; Pred. No. 8.8e0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY34133 standard; protein; 411 AA
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         100.0%;
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Best Local Similarity 100.
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                                                                                                                               MAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVVLYLII
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                                                  0; Indels
Score 2095; DB 2;
Pred. No. 2.9e-209;
1; Mismatches 0;
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  99.8%;
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                                                    Matches 410; Conservative
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                           Local Similarity
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(first entry)

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Homo sapiens
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            19-MAR-2001
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                                                                                                                                                                                                                                                                                                           This sequence is the h-TREX1 polypeptide, encoded by the h-TREX1 polynucleotide AAZ00039. h-TREX1 is a two pore potassium channel, and the gene maps to human chromosome 1q32, between the markers D18237 and W15105. The polynucleotide sequence of h-TREX1 can be used to diagnose a disease or susceptibility to a disease related to expression or activity of h-TREX-1 polypeptides. The methods of diagnosis may be used in the treatment of diseases including cancer, pulmonary, cardiovascular, and inflammatory diseases, pain, psychiatric disorders including depression and schizophrenia, neurodegenrative diseases including Alzheimer's, stroke, and head trauma and neurological disorders including migraine
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                                                                                                                                                                                                                                           New two pore potassium channel used for, e.g. treatment of pulmonary, cardiovascular and inflammatory diseases.
                                                                                                                                                                                                                                                                                    Claim 3; Page 24; 44pp; English
                                                                                                                                        (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                            98EP-00300570.
                                                                 98WO-EP007805
                                                                                                                                                                   Chapman CG
                                                                                                                                                                                              WPI; 1999-469126/39.
N-PSDB; AAZ00039.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 411 AA;
                                                                 02-DEC-1998;
                                                                                            27-JAN-1998;
09-OCT-1998;
                                    29-JUL-1999
                                                                                                                                                                    Meadows HJ,
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The present sequence is human TREXI (h-TREXI). h-TREXI is a member of the 2P domain potassium channel family of proteins which play a part in the control of fresting membrane potential. Modulation of these channels will therefore affect neuronal excitability, thereby leading to a modulation of neurotransmitter release and activity of neuronal networks. Such modulation therefore may be useful for the treatment of certain neurological conditions such as epilepsy, sleep-related disorders, cognitive dysfunction, attention deficit disorder, addiction, anxiety/phobia, Parkinson's and Huntington's chorea, cerebral palsy, incontinence, erectile dysfunction or alopecia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of human TREK1 polypeptide, polynucleotides encoding them and modulators of h-TREK1 polypeptides for treating epilepsy, sleep-related disorders, addiction and dyskinesias including Parkinson's and Huntington's chorea.
                            neuronal excitability; neurotransmitter release modulation; epilepsy; neurological disorder; sleep-related disorder; cognitive dysfunction; attention deficit disorder; addiction; anxiety; phobia; Parkinadov's chorea; Huntington's chorea; cerebral palsy; incontinence; erectile dysfunction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQIVAAINAGIIPLGNT
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potassium channel; resting membrane potential; neurotransmitter release modulation; epilepsy;
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Pred. No. 2.9e-209;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hervieu GJ, Meadows HJ, Randall AD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 7; Page 29; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                   erectile dysfunction; alopecia
                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2000; 2000WO-GB002107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99GB-00012733.
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Matches 410, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAC90412.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 411 AA;
                                                                                                                                                                                                                                                                                                  WO200072863-A2
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AAB50044 standard; protein; 411

AAB50044;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel isolated GPCR (G-protein coupled receptor) nucleic acid molecule. The polymucleotide and polympetide of the invention demonstrate neuroprotective, nootropic, tranquiliser, antimidratine, neuroleptic, antimanic, antidepressant, anticonvulsant, antimidratine, neuroleptic, antimanic, antidepressant, anticonvulsant, antiparkinsonian, cytostatic, cardiant, hypotensive, antianginal, antidepressant concertic, anti-HIV, antisathmatic, osteopathic, uropathic, antiulcer and antiallergic properties. The nucleic acid molecule and polypeptide of the invention may be useful in diagnosing, preventing, treating or ameliorating a medical condition, such as a disorder related to aberrant G-protein coupled signalling, a disorder related to aberrant G-protein coupled signalling, a disorder related to aberrant call disorders, severe mental retardation and dyskinesias, prain disorders, spinal cord disorders, immunological disorders, endocrimal diseases, growth disorders, immune-related disorders, endocrimal diseases, growth disorders, immune-related disorders, endocrimal diseases, growth chisorders, and pituitary disorders. Furthermore, the polynucleotide may be used in chromosome identification, in identifying organisms from minute current sequence is that of a human GPCR (G-protein coupled receptor) protein of the invention which was used for homology purposes.
                   tranquiliser; antimigraine; neuroleptic; antimanic; antidepressant; anticonvulsant; antiparkinsonian; cytostatic; cardiant; hypotensive; anticonvulsant; antiparkinsonian; cytostatic; cardiant; hypotensive; antianginal; analgesic; ancrectic; antiantimatic; osteopathic; evere mental retardation; dyskinesia; brain; spinal cord; affective; neoplastic; cardiovascular; immunological; immune; endocrinal; growth; eating; HIV infection; cancer; metabolic; pituitary; chromosome identification; gene therapy; human; receptor; potassium channel subfamily K member 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid molecule encoding a human G-protein coupled receptor, useful for diagnosing, preventing or treating diseases involving the receptor, e.g. Parkinson's disease, dementia, asthma, hypertension or
 KKTKEEVGEFRAHAAEWTANVTAEFKETRRLSVEIYDKFQRATSIKRKLSAELAGNHNO
                                                                                           411
                                                                                                                                                                                                                                                                                                    coupled receptor; neuroprotective; nootropic;
                                                                              361 ELTPCRRTLSVMHLTSERDVLPPLLKTESIYLNGLTPHCAGEEIAVIENIK
                                                               ELTPCRRTLSVNHLTNERDVLPPLLKTESIYLNGLTPHCAGEEIAVIENIK
                                                                                                                                                                                                                                                                       Human GPCR potassium channel, subfamily K, member 2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Feder JN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; SEQ ID NO 31; 224pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gopal S, Mintier G,
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                                                                                                                                                                          ADP03586 standard; protein; 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BRIM ) BRISTOL-MYERS SQUIBB CO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-JAN-2003; 2003WO-US001911
                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                      G-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2003062393-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ramanathan CS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                               361
                                                                                                                                                                                                         ADP03586;
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                                                                                                                                          RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is that of the human two pore domain K+ channel TREK
                                                                                                                                                                                  120
                                                                                                                                                                                                        SNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180
                                                                                                                                                                                                                                                                                240
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                                                                                                                                                                                                                                                                                                                                                                                                                                     AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSIKRKLSAELAGNHNQ 360
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                                                                                                                                                                                  GATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQIVAAINAGIIPLGNT
                                                                                                                                                                                                                                                                                                                                      LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAIIFKHIEGWSALD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TREK-1; sleep; two pore domain potassium channel; sedative; hypnotic;
                                                                     Gaps
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                                                                     Indels
                                  Length
                                 Score 2095; DB 7;
Pred. No. 2.9e-209;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human two pore domain potassium channel TREK-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADQ76698 standard; protein; 411 AA
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                                 99.8%;
99.8%;
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                                                                       Matches 410; Conservative
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                                                    Local Similarity
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Sequence 411 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADQ76698;
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                                 Query Match
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/note= "M4 membrane spanning segment"

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ADP03575 standard; protein; 422
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-1. In rate, TREK-1 is highly expressed in much of the brain and is inhibited by protein kinase C and protein kinase C mediated phosphorylation. It is activated by volatile general anaesthetics and is expressed at high levels in the brain of sleep animals. Based on these criteria and on experimental results, it is hypothesized that TREK-1 is a key mediator of sleep (when open) and waking (when closed). The invention provides methods for identifying a sleep-or wakefulness-promoting compound based on the compound's ability to modulate two pore domain K+channels such as TREK-1. It also provides screening methods for isolating short sleep, no rebound and sleep deprivation resistant Drosophila mutants useful for identifying sleep-related molecular targets.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; TWIK-Related K+ Channel-1; TREK-1; anaesthetic; screening
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                                                                                                                                                                                 99.8%; Score 2095; DB 8; Length 411; 99.8%; Pred. No. 2.9e-209; ive 1; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human TWIK-Related K+ Channel-1 (TREK-1) protein.
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/note= "M1 membrane spanning se /note= "P1 pore domain" 158. 178
/note= "M2 membrane spanning se 209. 230
/note= "M3 membrane spanning se 336. 259
/note= "P2 pore domain" 274. 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                Local Similarity 99.8
Hes 410; Conservative
                                                                                                                                                          Sequence 411 AA;
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Region
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The invention relates to a mammalian K+ channel protein with two pore domains, called TREK2 (TWIK-Related K+ Channel). The protein produces currents whose current-voltage relationship is slightly inwardly rectifying in high symmetrical K+ conditions. TREK2 is a member of fatty acid-activated and mechanosensitive K+ channel family. TREK-2 gene located on chromosome 14g31 is abundantly expressed in kindey, pancreas and moderately in testis, brain, colon and small intestine. The mammalian K+ channel protein is useful in methods for screening various compounds. In particular, the protein is useful in methods for identifying biologically active compounds with anaesthetic properties. The present sequence is TREK-1 protein used in the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New mammalian K+ channel protein with two pore domains, for screening various compounds, particularly for identifying biologically active compounds with anesthetic properties.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
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Pred. No. 6e-209;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 1A; 50pp; English
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27-JUN-2001; 2001US-00892360.
                                                                                                               27-JUN-2001; 2001WO-IB001436
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                                                                                                                                                                                                                                                                                                                      Lesage F,
                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-139903/18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 411 AA;
WO200200715-A2
                                                                                                                                                                                                                                                                                                                   Lazdunski M,
                                                      03-JAN-2002
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The invention relates to a novel isolated GPCR (G-protein coupled receptor) nucleic acid molecule. The polymucleotide and polypeptide of the invention demonstrate neuroprotective, nootropic, tranquiliser, antimigraine, neuroleptic, antimanic, antidepressant, anticonvulsant, antiparkinsonian, cytostatic, cardiant, hypotensive, antianginal, antiparkinsonian, cytostatic, cardiant, hypotensive, antianginal, analgesic, anorectic, anti-HIV, antiasthmatic, osteopathic, uropathic, analgesic, anorectic, properties. The mucleic acid molecule and polypeptide of the invention may be useful in diagnosing, preventing, treating or ameliorating a medical condition, such as a disorder related to aberrant G-protein coupled signalling, a disorder related to aberrant cell cycle regulation, neurological disorders, spinal cord disorders, immunological disorders, mophastic disorders, spinal cord disorders, immunological disorders, endocrinal diseases, immunological disorders, motabolic disorders and pituitary disorders. Furthermore, the polynucleotide may be used in chromosome identification, in identifying organisms from minute current sequence is that of a human GPCR (G-protein coupled receptor) protein which was isolated by the method of the invention.
                                                                                                                                                                      tranguiliser; antimigraine, peur; antimanic; antidepressant; anticonvulsant; antiparkinsonian; cytostatic; cardiant; hypotensive; antiangunai; antiparkinsonian; cytostatic; cardiant; hypotensive; antiangunai; antiasthmatic; osteopathic; uropathic; antiulcer; antiallergic; call cytole regulation; neurological; severe mental retardation; dyskinesia; brain; spinal cord; affective; neoplastic; cardiovascular; immunological; immune; endocrinal; growth; carting; HIV infection; cancer; metabolic; pituitary; chromosome identification; gene therapy; human; receptor; twin pore channel; potassium channel subfamily K member 2 variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid molecule encoding a human G-protein coupled receptor, useful for diagnosing, preventing or treating diseases involving the receptor, e.g. Parkinson's disease, dementia, asthma, hypertension or
                                                                                                          Human GPCR twin pore channel" protein variant "Gene 9" protein.
                                                                                                                                                        GPCR; G-protein coupled receptor; neuroprotective; nootropic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ramanathan CS, Gopal S, Mintier G, Feder JN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-JAN-2003; 2003WO-US001911.
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                                                              (first entry)
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Best Local Similarity 99.3
Matches 408; Conservative
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N-PSDB; ADP03564.
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                                                              29-JUL-2004
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                    ADP03575
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The invention relates to a mutant potassium ion channel protein, having four membrane spanning domains and two pore forming domains, comprising a mutation at the second pore forming domain. The expression of the mutant protein in a cell confers improved inward potassium flux and the ability to grow in the presence of potassium. Mutant proteins and their corresponding polymucleotide sequences can therefore be used to improve inward potassium flux into cells under acidic conditions by modulating the membrane potential using therapeutic agents. The sequences may be used to develop agenists and antagonists of potassium channel proteins in order to control peets such as nematodes and insects. This sequence represents a human transmembrane potassium ion channel proteins in
                                                                                                                         240
                                                             180
                                                                             SNOISHWDLGSSFFFAGTVITTIGFGNISPRIEGGKIFCIIYALLGIPLFGFLLAGVGDQ 191
                                                                                                                                                        251
                                                                                                                                                                                       AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS 300
GATVFKALEOPHEISORTTIVIOKOTFISOHSCVNSTELDELIQQIVAAINAGIIPLGNT 120
                 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFORATSIKRKLSAELAGNHNQ 360
                                                                                                                                                                                                                                                                     Transmembrane potassium ion channel protein; inward potassium flux; pest control; membrane potential; pesticide; antihelminthic; nematode;
                                                                                                                                             LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIPILFGCVLFVALPAIIFKHIEGWSALD
                                                             SNOISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ
                                                                                                                         LGTI FGKGIAKVEDTFIKMNVSQTKIRIISTIIFILFGCVLFVALPAIIFKHIEGWSALD
                                                                                                                                                                                                         New polypeptide, a mutant potassium ion channel protein for improving inward potassium flux under acidic conditions.
                                                                                                                                                                                                                                                                                                                411
                                                                                                                                                                                                                                                                                                                ELIPCRRILSVNHLINERDVLPPLLKTESIYLNGLTPHCAGEEIAVIENIK
                                                                                                                                                                                                                                                                                                                                 Human potassium ion channel TPKC1 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  insect; TPKC1; human.
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Claim 37; Page 113-115; 131pp; English.
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Misc-difference 272
                                                                                                                                            Sequence 426 AA;
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                                                                   16 VAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVVLYLII
                                                                                                                                  SNOISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ
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                                                                                            GATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQIVAAINAGIIPLGNT
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                                                        1 MAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVVLYLII
                                                                                                           76 GATVPKALEQPHEISQRITIVIQKQTFISQHSCVNSTELDELIQQIVAAINAGIIPLGNT
                                      Gaps
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                  Length 426;
                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                   Human potassium ion channel TPKC1 mutant protein #1.
                 Score 2062; DB 4;
Pred. No. 8.5e-206;
3; Mismatches 3;
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                   98.2%;
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                           Best Local Similarity 98.5
Matches 405; Conservative
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Misc-difference 256
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Sequence 426 AA;
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                   Query Match
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four membrane spanning domains and two pore forming domains, comprising a mutation at the second pore forming domain. The expression of the mutant protein in a cell confers improved inward potassium flux and the ability to grow in the presence of potassium. Mutant proteins and their corresponding polynucleotide sequences can therefore be used to improve inward potassium flux into cells under acidic conditions by modulating the membrane potential using therapeutic agents. The sequences may be used to develop agonists and antagonists of potassium channel proteins in order to control pests such as memarodes and insects. This sequence
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The invention relates to a mutant potassium ion channel protein, having
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATVFKALEQPHEISORTTIVIOKOTFISOHSCVNSTELDELIQQIVAAINAGIIPLGNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELTPCRRTLSVNHLTNERDVLPPLLKTESIYLNGLTPHCAGEEIAVIENIK 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98.0%; Score 2058; DB 4; 98.3%; Pred. No. 2.2e-205; ive 3; Mismatches 4;
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Homo sapiens
                                                                                                                                                                         23-AUG-2001
                                                                                                                                                                                                                                                                          Pausch MH;
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                                                                                                                                                                                                                       four membrane spanning domains and two pore forming domains, comprising a mutation at the second pore forming domain. The expression of the mutant protein in a cell confers improved inward potassium flux and the ability to grow in the presence of potassium. Mutant proteins and their corresponding polynucleotide sequences can therefore be used to improve inward potassium flux into cells under acidic conditions by modulating the membrane potential using therapeutic agents. The sequences may be used to develop agonists and antagonists of potassium channel proteins in order to control pests such as nemacodes and insects. This sequence represents a human transmembrane potassium ion channel TPKCI mutant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 VAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVVLYLII
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                                                                                                                                                                                                              channel protein,
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                                                                                                                                                                                                                                                                                                                                                                                                 98.0%; Score 2057; DB 4;
98.3%; Pred. No. 2.8e-205;
ive 4; Mismatches 3;
                                                                                                                                                                                                              to a mutant potassium ion
                                                                                                                                                                                      Claim 37; Page 115-117; 131pp; English.
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            14-FEB-2001; 2001WO-US004680
                                     15-FEB-2000; 2000US-00503849
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                                                                                                                                                                                                              invention relates
                                                                                                             WPI; 2001-536570/59.
N-PSDB; AAS12182.
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les 404; Conserv
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                                                                                                                                                  New polypeptide,
inward potassium
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                                                              (BADI ) BASF
                                                                                      Pausch MH;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                 Transmembrane potassium ion channel protein; inward potassium flux; pest control; membrane potential; pesticide; antihelminthic; nematode; insect; TPKC1; human; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polypeptide, a mutant potassium ion channel protein for improving inward potassium flux under acidic conditions.
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                                                                                                                                                                                                                                                                                      /note= "Wild-type Gly replaced by Arg
Human potassium ion channel TPKC1 mutant protein #4.
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Pred. No. 5.8e-205;
3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 37; Page 119-120; 131pp; English
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                                                                                                                                                                                                                                 Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                          WO200161006-A2
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256 AIYEVVITLTTIGFGDHVVGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGRLVRVIS 315
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SNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ
                                                                                             LGTIFGKGIAKVEDTFIKWNVSQTKIRISTIIFILFGCVLFVALPAIIFKHIEGWSALD
                                                                                                           196 LGTIFGKGIAKVEDTFIKWNVSQTKIRISTIIFILFGCVLFVALFAIIFKHIEGWSALD
                                                                                                                                                                                                        KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSIKRKLSAELAGNHNQ
                                                                                                                                                  AIYFVVITLTTIGFGDYVAGGSDIBYLDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS
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                                                                                                                                                                                                                                                                            ELTPCRRTLSVNHLTSERDVLPPLLKTESIYLNGLAPHCAGEBIAVIENIK 426
                                                                                                                                                                                                                                                            ELTPCRRTLSVNHLTNERDVLPPLLKTESIYLNGLTPHCAGEEIAVIENIK 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        four membrane spanning domains and two pore forming domains, comprising a mutation at the second pore forming domain. The expression of the mutant protein in a cell confers improved inward potassium flux and the ability to grow in the presence of potassium. Mutant proteins and their corresponding polymuclachies sequences can therefore be used to improve inward potassium flux into cells under acidic conditions by modulating the membrane potential using therapeutic agents. The sequences may be used to develop agonists and anteagonists of potassium channel proteins in order to control pests such as nematodes and insects. This sequence represents a human transmembrane potassium ion channel TPKCI mutant
 316 KKTKEEVGEFRAHAAEWTANVTAEFKETRRLSVEIYDKFQRATSIKRKLSAELAGNHNQ 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a mutant potassium ion channel protein, having
                                                                                                                                                                                                                              Transmembrane potassium ion channel protein; inward potassium flux; pest control; membrane potential; pesticide; antihelminthic; nematode; insect; TPKC1; human; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polypeptide, a mutant potassium ion channel protein for improving inward potassium flux under acidic conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 VAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVVLYLII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVVLYLII
                                          376 BLTPCRRTLSVNHLTSERDVLPPLLKTESIYLNGLAPHCAGEBIAVIBNIK 426
                            ELTPCRRTLSVNHLTNERDVLPPLLKTESIYLNGLTPHCAGEEIAVIENIK 411
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                                                                                                                                                                                                                                                                                                                                             'note= "Wild-type Tyr replaced by His"
                                                                                                                                                                                                                                                                                                                                                                       /note= "Wild-type Ala replace by Val"
                                                                                                                                                                                                        Human potassium ion channel TPKC1 mutant protein #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 2053; DB 4;
Pred. No. 7.4e-205;
4; Mismatches 4;
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                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                        $
                                                                                                                       AAU07624 standard; protein; 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-FEB-2001; 2001WO-US004680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-FEB-2000; 2000US-00503849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97.8%;
ilarity 98.1%;
Conservative
                                                                                                                                                                             (first entry)
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les 403, Conserv
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                                                                                                                                                                                                                                                                                                                                                           Misc-difference
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                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                              21-NOV-2001
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The invention relates to human and mouse TREK-1 potassium channel proteins and their corresponding DNA molecules. TREK-1 nucleic acid is useful for transfecting cells to induce expression of the TREK-1 potassium channel protein. These cells are then used in assays to identify compounds which have anaesthetic properties, producing a safe, reversible state of unconsciousness with concurrent amnesia and analgesia in a mammal upon inhalation. The present sequence is murine TREK-1
Novel nucleic acid encoding a TREK-1 potassium channel protein for transfecting cells to be used to identify compounds with anesthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 411;
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61 GATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQIVAAINAGIIPLGNT 120

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                                                                                                                                                                                                                                                  KKTKEEVGEFRAHAAEWTANVTAEFKETRRLSVEIYDKFQRATSIKRKLSAELAGNHNQ 360
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                                                                                      GAAVFKALEQPQEISORTTIVIOKOTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS
                                                                                                                                SNQVSHWDLGSSFFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ
                                                                                                                                                                           AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS
                                                                                                                                                                                                                    AIYFVVITITITITIGEGDYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS
                                                                                                                                                                                                                                                               KKTKEEVGEFRAHAAEWTANVTAEFKETRRILSVELYDKFORATSVKRKLSAELAGNHNO
                                                   1 MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVVLYLII
                                                                          GATVFKALEQPHEISORTTIVIOKOTFISOHSCVNSTELDELIQQIVAAINAGIIPLGNT
                                                                                                                     SNOISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDO
                                                                                                                                                              LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAIIFKHIEGWSALD
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            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           two pore potassium channel; inflammatory disease;
           Indels
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 No. 1.3e-203
          12; Mismatches
Pred.
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                                                                                                                                                                                                                                                                                                                                                                       AAY28497 standard; protein; 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SMIK ) SMITHKLINE BEECHAM PLC.
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 96.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse h-TREK1 polypeptide
Best Local Similarity 96.1
Matches 395; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chapman CG
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N-PSDB; AAZ00040.
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09-OCT-1998;
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 and inflammatory
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diseases including cancer, pulmonary, cardiovascular, and infla diseases, pain, psychiatric disorders including depression and schizophrenia, neurodegenerative diseases including Alzheimer's and head trauma and neurological disorders including migraine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 411;
                                                                                                                                                             Indels
                                                                                                                      Score 2035; DB 2;
Pred. No. 5.3e-203;
2; Mismatches 5;
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                                                                                                                        Query Match
Best Local Similarity 95.9%; Pre
Matches 394; Conservative 12;
                                                                                        Sequence 411 AA;
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Copyright (c) 1993 - 2005 Compugen Ltd.
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July 13, 2005, 08:01:55; Search time 93.9622 Seconds (without alignments) 2239.886 Million cell updates/sec Run on:

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score: Perfect Title:

2100 1 MAAPDLLDPKSAAQNSKPRL......LNGLTPHCAGEEIAVIENIK 411 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 seqs, 512079187 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

UniProt 03:* Database

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Q9nrt2 homo sapien	bos t	O95069 homo sapien	_	_		Q6q834 oryctolagus	Ospzpo m mns mnscn	_	Q9jis4 rattus norv				Q9nyg8 homo sapien	-	Q924i4 rattus norv	m mus	homo	homo	homo	homo	homo	brack	095279 homo sapien		Q9jk62 m potassium			homo	4 homo s	Q8r454 cavia porce
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* Query Match	99.8	99.0	98.2	97.2	97.2	96.4	59.7	59.5	59.5	59.5	59.2	59.5	58.0	38.2	37.0	36.4	29.3	24.6	23.9	23.6	21.7	21.4		20.3		19.6	19.5	19.4	19.0	18.7	18.1
Score	2095	2079	2062	2042	2041	2025	1254	1250	1249.5	1249	1243	1243	1217.5	803	776.5	764.5	919	516.5	502.5	496.5	456	450	432.5	427	413	412.5	409.5	406.5	400	393	380
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O00180 homo sapien Q9z2tz rattus norv O99199 mus musculu	Qaavis xenopus lae O08581 mus musculu O14649 homo sapien	Q9j158 cavia porce O02821 oryctolagus Q6peil brachydanio	Q923v6 rattus norv Q9ngc2 homo sapien Q63zi0 xenopus lae Q9y257 homo sapien	Q9h427 homo sapien
CIW1_HUMAN Q9Z2T2 0991,99	QBAVIS CIW1_MOUSE CIW3_HUMAN	CIW9_CAVPO 002821 Q6PE11	Q923V6 CIW9 HUMAN Q63ZIO CIW6 HUMAN	CIWF_HUMAN
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336 336	331 336 346	365 323	396 374 374	330
18.1	17.7	17.0 17.0 16.9	16.7 16.6 16.6 16.6	16.5
379.5	372 370.5 363	357.5 356.5 355	351.5 349.5 348.5 348	347.5
288	365	8 6 6 6 6 0	4 4 4 4	45

ALIGNMENTS

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TISSUENCE FROM N.A.

TISSUEPCR rescued clones;

TISSUEPCR rescued clones;

MEDLINE-22388257; PubMed=1247932; DOI=10.1073/pnas.242603899;

ALTSUEPCR PROJECT B. Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar N.K.,

Hopkins R.F., Jordan H., Moore T. Max S.I., Wang J., Hable R.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., WcEwan P.J., McKernan K.J., Malk Y.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mhiting M., Madan A., Young A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.,

Jones S.J., Marra M.A.,

The man initial analysis of more than 15,000 full-length human
                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Two-pore domain potassium channel TREK-1 (Potassium channel, subfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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TISSUE=PCR rescued clones;
Strausberg R.;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.8) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=2024,931; PubMed=10784345;
Meadows H.J., Benham C.D., Cairns W., Gloger I.S., Jennings C.,
Medhurst A.D., Murdock P., Chapman C.G.;
"Cloning, localisation and functional expression of the human
orthologue of the TREK-1 potassium channel.";
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                                                                                  411 AA.
                                                                                                                                                                Created)
                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                        K, member 2).
Name=TREK-1; Synonyms=KCNK2;
                                                                                                                                                        (TrEMBLrel. 15, (TrEMBLrel. 15,
                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                01-OCT-2000
                                                                                                                           Q9NRT2
                                                                                  Q9NRT2
RESULT 1
Q9NRT2
                                                                                      HIDDELLIND THE SERVICE SERVICE
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Best Local Similarity 99.0
Matches 407; Conservative
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                                                                                                                        Ion transport;
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                                                                                                                                                                                                          Gaps
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TISSUB-Adrenal cortex;
MEDLINE=22379553; PubMed=12368289; DOI=10.1074/jbc.M207233200;
BRDLINE=223799553; PubMed=12368289; DOI=10.1074/jbc.M207233200;
BRYGART J.G., Xu L., Danthi S., Enyeart J.A.;
"An ACTH- and ATP-regulated background K+ channel in adrenocortical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Biol. Chem. 277:49186-49199(2002).
-!- SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.8) family.
EMBL, AY148447, AAN37591.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          411
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                                                                                                                                                                            99.8%; Score 2095; DB 2; Length 411; 99.8%; Pred. No. 1.7e-133; ive 1; Mismatches 0; Indels (
                                                                                                                                             ionic channel; Transmembrane; Transport
AA; 45494 MW; FDE40CAB21B42A1C CRC64;
EMBL; AF171068; AAF89743.1; -.
EMBL; BC069462; AAH69463.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0005216; F:ion channel activity; IEA.
GO; GO:0005216; F:ion channel activity; IEA.
GO; GO:0006811; P:ion transport; IEA.
GO; GO:006813; P:potassium ion transport; IEA.
InterPro; IPR003280; K+channel 2pore.
InterPro; IPR001622; K+channel 2pore.
InterPro; IPR01333; ZPOREKCHANEL.
PRINTS; PR01333; ZPOREKCHANEL.
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Last sequence update)
Last annotation update)
K member 2.
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                                                                                                                                                                              Query Match
Best Local Similarity 99.8
Matches 410, Conservative
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Potassium channel subfamily K member 2 (Outward rectifying potassium
channel protein TREK-1) (TREK-1 K+ channel subunit) (Two-pore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99254548; PubMed=10321245; DOI=10.1038/8084; Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.; "Inhalational anesthetics activate two-pore-domain background K+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name-KCNK2; Synonyms-TREK, TREK1;
Homo sapions (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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TISSUBERAIN;
Price L.A., Hellings S.E., Hayashi J.H., Pausch M.H.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                   Transport.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0005216; F:ion channel activity; IEA.
GO; GO:000527; F:potassium channel activity; IEA.
GO; GO:0006811; P:ion transport; IEA.
GO; GO:0006811; P:ion transport; IEA.
InterPro; IPR003280; K+channel_zpore.
InterPro; IPR003280; K+channel_zpore.
InterPro; IPR00376; Trek_channel.
FRINTS; PR01333; 2POREKCHANNEL.
PRINTS; PR01399; TREKCHANNEL.
                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                ort; Ionic channel; Transmembrane; Tra
411 AA; 45438 MW; A185EAC20A68CCDC
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                                                                                                                                                                                                                                                                                                                                            99.0%; Score 2079; D 99.0%; Pred. No. 2e-1:ive 2; Mismatches
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Query Match
Best Local Similarity 96.1;
Matches 395; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                     Kcnk2 protein,
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                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                 -!- SUBUNIT: Homodimer (Potential).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- MISCELLANEOUS: Activated by volatile general anaesthetics such as chloroform, halothane and isoflurane.
-!- SIMILARITY: Belongs to the two pore domain potassium channel
(TC 1.A.1.8) family.
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GG; GO:0016207; C:membrane; NAS.
GG; GO:0016271; F:outward rectifier potassium channel activity; NAS.
GG; GO:0016271; F:outward rectifier potassium channel activity; NAS.
GG; GO:0006913; P:potassium ion transport; NAS.
InterPro; IPR0036976; K-channel_pore.
InterPro; IPR003976; Trek_channel_pore.
InterPro; IPR003976; Trek_channel_pore.
InterPro; IPR003976; Trek_channel_pore.
GIYCOPTOCOEin; Ion transport; Ionic channel; Potassium;
Potassium channel; Transmembrane; Transport; Voltage-gated channel.
DOWAIN

1 61 CYtoplasmic (Potential).
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Essential for chloroform and halothane
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Required for basal channel activity (By Similarity).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
Missing (in Ref. 2).
RLV -> DWL (in Ref. 2).
S -> N (in Ref. 2).
A -> T (in Ref. 2).
A -> T (in Ref. 2).
A -> T (in Ref. 2).
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Cytoplasmic (Potential).
Potential.
  FUNCTION: Outward rectifying potassium channel.
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                                                                                                                                                                                                                                                                                                                                 EMBL; AF129399; AAD47569.1; -. EMBL; AF004711; AAD01203.1; -.
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411
426 AA;
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RN SEQUENCE FROM N.A.

STRAUBBERGE R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Distribenco L., Marusdina K., Farmer A.A., Rubin G.M., Hong L.,

RA Distribenco L., Marusdina K., Farmer A.A., Rubin G.M., Hong L.,

RA Distribenco M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Ugdin T.B., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Holton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Maring M., Schwutz J., Myers R.M., Butterfield Y.S.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Jones S.J., Marra M.A.;

RA Jones S.J., Walle A., 99:16899:16903(2002).
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256 AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGRLVRVIS 315
                                                                                  KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSIKRKLSAELAGNHNQ 360
                                                                                                                          316 KKTKEEVGEFRAHAAEWTANVTAEFKETRRISVEIYDKFQRATSIKRKLSAELAGNHNQ 375
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.

-1- SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.8) family.

EMBL; BC062094; AM462094.1; -.

GO; GO:016021; C:integral to membrane; TAS.

GO; GO:00016021; C:volteage-gated potassium channel activity; IDA.

GO; GO:000186; P:voltage-gated potassium channel activity; IDA.

GO; GO:0007186; P:G-protein coupled receptor protein signalin.

GO; GO:0007186; P:G-protein coupled receptor protein signalin.

GO; GO:00030322; P:stabilization of membrane potential; TAS.
                                                                                                                                                                                                                                                                                                        376 ELTPCRRTLSVMHLTSERDVLPPLLKTESIYLNGLAPHCAGEEIAVIENIK 426
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PRINTS; PR01499; TREKCHANNBL.
Ion transport; Ionic channel; Transmembrane; Transport.
SEQUENCE 414 AA; 45555 MW; 27F52D51DFFC66F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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96.1%; Pred. No. 6.5e-130;
ive 13; Mismatches 3;
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InterPro; IPR001622; K+channel_pore.
InterPro; IPR003976; Trek_channel.
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STRAIN=C57BL/6; TISSUE=Brain;
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                                                                                                       SHILLDPKSAAQUSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVVLYLII
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                                                                                       GATVFKALEOPHEISORTTIVIOKOTFISOHSCVNSTELDELIQQIVAAINAGIIPLGNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-UTL-2004 (Rel. 44, Last annotation update)
Potassium channel subfamily K member 2 (Outward rectifying potassium channel protein TREK-1) (Two-pore potassium channel TREK-1) (TREK-1 K+ channel subunit).
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Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
"Inhalational anesthetics activate two-pore-domain background K+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -I- FUNCTION: Outward rectifying potassium channel.
-I- SUBMIT: Homodiner (Potential).
-I- SUBMIT: Homodiner (Potential).
-I- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-I- TISSUE SPECIFICITY: High expression in brain and lung. Also detected in kidney, heart and skeletal muscle. Not detected in liver. In the brain, highest expression in olfactory bulb, hippocampus and cerebellum.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning, functional expression and brain localization of a novel unconventional outward rectifier K+ channel."; EMBO J. 15:6854-6862(1996).
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Lazdunski M.;
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BrbILNE=97157476; PubMed=9003761;
Fink M., Duprat F., Lesage F., Re;
Lazdunski M.;
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Nat. Neurosci. 2:422-426(1999)
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIFILFGCVLFVALPAIIFKHIEGWSALD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVVLYLII
MISCELLANEOUS: Inhibited by barium. Activated by volatile general anaesthetics such as chloroform, diethyl ether, halothane and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytoplasmic (Potential).
Essential for chloroform and halothane
                                                                                                                                                                                                                                                                                     EMBL, U73488; AAC53005.2; --
MGD; MGI:109366; Kcnk2.
GO; GO:008076; C:voltage-gated potassium channel complex; IDA.
GO; GO:006224; F:voltage-gated potassium channel activity; IDA.
GO; GO:006249; F:voltage-gated potassium channel activity; IDA.
GO; GO:0007186; P:potassium ion transport protein signalin.
InterPro; IPR003280; K+channel_pore.
InterPro; IPR001622; K+channel_pore.
PRINTS; PR01333; 2POREKCHĀNEL.
PRINTS; PR01499; TREKCHĀNBEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Required for basal channel activity.
N-linked (GlcNac. .) (Potential).
N-linked (GlcNac. .) (Potential).
                                      isoflurane.
SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.8) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELTPCRTLSVNHLTNERDVLPPLKTESIYLNGLTPHCAGEEIAVIENIK 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR01499; IKENCHANNIEL.
Glycoprotein; Ion transport; Ionic channel; Potassium;
Potassium channel; Transmembrane; Transport; Voltage-gated (DOMAIN 1 46 Cytoplasmic (Potential).

TRANSMEM 47 67 Potential.

TRANSMEM 129 155 Pore-forming 1 (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Potential.
Cytoplasmic (Potential).
Potential.
Pore-forming 2 (Potential).
Potential.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 2041; DB 1, NO. 7.6e-130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 7.6e
12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sensitivity.
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Best Local Similarity 96.1
Matches 395; Conservative
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1155
1177
2207
228
268
293
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95
119
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119
411 AA;
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SEQUENCE
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296 LRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSIKRKLSAELA 355
  196 LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAVIFKHIEGWSALD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59844 MW; 1F06C8EA0DE8CB4D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 1254; DB 2;
; Pred. No. 1.4e-76;
56; Mismatches 63
                                                                                                                                                                                                                                                                                                                                            538
                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 63.7°
Matches 247; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              Potassium channel TREK-2.
                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             538 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=KCNK10;
                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004
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Q6Q834;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNOISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Wistar;
MEDLINE=21896087; PubMed=11897838;
Gu W., Schlichthorl G., Hirsch J.R., Engels H., Karschin C.,
Karschin A., Derst C., Steinlein O.K., Daut J.;
"Expression pattern and functional characteristics of two novel splice variants of the two-pore-domain potassium channel TREK-2.";
J. Physiol. 539:657-668(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQIVAAINAGIIPLGNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVVLYLII
                                                                                                                                                                                                                                                                                                                                                                                                                                          Bockenhauer D., Zilberberg N., Goldstein S.A.; "KCNK2: reversible conversion of a hippocampal potassium leak into
                                                                                                                      01-DEC-2001 (TEMBLrel. 19, Last sequence update)
25-OCT-2004 (TEMBLrel. 19, Last sequence update)
2P domain potassium channel KCNK2 (Tandem pore domain potassium channel KCNK2 (Tandem pore domain potassium potassium channel).
ELTPCRRTLSVNHLTSEREVLPPLLKAESIYLNGLTPHCAGEDIAVIENMK 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 96.4%; Score 2025; DB 2; Best Local Similarity 95.4%; Pred. No. 9.4e-129; Matches 392; Conservative 11; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ionic channel; Transmembrane; AA; 46912 MW; CACDA05BBE95FD
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                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21219399; PubMed=11319556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neurosci. 4:486-491(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   voltage-dependent channel."
                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
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SEQUENCE 426 AA;
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Brain;
361
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                               KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFORATSIKRKLSAELAGNHNO 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 VGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPALIFKHIEGW
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Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
L. Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-1- SINILARITY: Belongs to the two pore domain potassium channel
(TC 1.A.1.8) Family.
R GO: 60:001601; C:integral to membrane; IEA.
R GO: 60:001621; C:integral to membrane; IEA.
R GO: 60:001621; F:ion channel activity; IEA.
R GO: 60:000611; F:ion transport; IEA.
R GO: 60:0006811; P:potassium ion transport; IEA.
R GO: 60:0006813; P:potassium ion transport; IEA.
R InterPro; IPR001280; K+channel_2pore.
R InterPro; IPR00122; K+channel_pore.
R InterPro; IPR001996; Trek_channel.
R RRINTS; PR01499; TREKCHANNEL.
R PRINTS; PR01499; TREKCHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                         ELTPCRRTLSVNHLTNERDVLPPLLKTESIYLNGLTPHCAGEBIAVIENIK 411
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Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:9630032C21 product:POTASSIUM CHANNEL SUBFAMILY K MEMBER 10 (OUTWARD RECTIFYING POTASSIUM CHANNEL PROTEIN TREK-2) (TREK-2 K+ CHANNEL SUBUNIT) homolog (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C5701/6J; TISSUB=Cerebellum; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y., Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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STRAIN=C57BL/6J; TISSUE=Cerebellum;
STRAIN=C57BL/6J; TISSUE=Cerebellum;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Saaaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsunoto H., Sakaguchi S., Ikagami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watchiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatau M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                  STRAIN=CS7BL/66; TISSUE=cerebellum; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Rayashizaki Y.; High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CS7BL/6J; TISSUB=Cerebellum;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDNAs.";
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                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CS7BL/6J; TISSUE=Cerebellum;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                            356 GNHNQELTPCRRTLSVNHLTNERDVLPP 383
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                                                                                                                                           PRELIMINARY;
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Nature 420:563-573(2002)
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 24, Last sequence update)
01-WAR-2003 (TrEMBLrel. 24, Last annotation update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length enriched
library, clone:C230015H11 product:POTASSIUM CHANNEL SUBFAMILY K MEMBER
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Matches 255; Conservative
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STRAIN-C57BL/6J; TISSUE-Cerebellum;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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                                                                                                                 SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Cerebellum;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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10 (OUTWARD RECTIFYING POTASSIUM CHANNEL PROTEIN TREK-2) (TREK-2 K+CHANNEL SUBUNIT) homolog.
                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                   "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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STRAIN=C57BL/6J; TISSUE=Cerebellum;
MEDLINE=20499374; Pubmed=11042159; DOI=10.1101/gr.145100;
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE=Cerebellum;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
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Genome Res. 10:1757-1771(2000).
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GO:0005216; F:ion channel activity; IEA.
GO:0005267; F:potassium channel activity; IEA.
GO:0006811; P:ion transport; IEA.
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AK082153; BAC38424.1; -.
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                                 Mus musculus (Mouse)
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                                                                             NCBI_TaxID=10090;
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79 YLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHICVSPQELETLIQHALDADNAGVSP 138
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16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Potassium channel subfamily K member 10 (Outward rectifying potassium channel protein TREK-2) (TREK-2 K+ channel subunit).
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                     35,
                                                                                                                                                                                                                                                                                      DB 2; Length 535;
                                                                                                                                                                                                                                                                                                                                                     77; Indels
                                                                                                                                                                                      Ion transport; Ionic channel; Transmembrane; Transport.
SEQUENCE 535 AA; 59401 MW; 3E99E89F875C26BD CRC64;
                                                                                                                                                                                                                                                                                                                           Pred. No. 2.8e-76;
      GO:0006813; P:potassium ion transport; IEA.
                                                                                                                                                                                                                                                                                      59.5%; Score 1249.5;
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GO; GO:0006813; P:porabblum Luncarporers InterPro; IPR003280; K+channel_Zpore. InterPro; IPR001622; K+channel_pore. InterPro; IPR003976; Trek_channel.
                                                                                                                          PRINTS; PR01333; 2POREKCHĀNEL.
PRINTS; PR01499; TREKCHĀNNEL.
                                                                                                                                                                                                                                                                                                                       59.38;
                                                                                                                                                                                                                                                                                                                                                  Matches 252; Conservative
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                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 YLIIGATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQIVAAINAGIIP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRLSVBIYDKFORATSIKRKLSAELA 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 AAPDLLDPKSA--AQNSKPRLSFSTKPTVLASRVESDT---TINVMKWKTVSTIFLVVVVL 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 AAPPVCQPKSATNGHHPVPRLSISSRATVVA-RMEGASQGGLQTVMKWKTVVAIFVVVVV 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SALDAIYFVVITLTTIGFGDYVAGG-SDIBYLDFYKPVVWFWILVGLAYPAAVLSMIGDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177 VGDQLGTIFGKGIAKVEDTFIKMNVSQTKIRIISTIIFILFGCVLFVALPAIIFKHIEGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                               Glycoprotein; Ion transport; Ionic channel; Potassium;
Potassium channel; Transmembrane; Transport; Voltage-gated channel.
             SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.8) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytoplasmic (Potential).
N-linked (GlcNAc. . ) (Potential)
N-linked (GlcNAc. . .) (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64; Indels 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59.5%; Score 1249; DB 1; Length 538; 63.7%; Pred. No. 3.1e-76;
                                                                                                                                                                                                                                                                                                                                                          Potential.

Cytoplasmic (Potential).

Potential.

Potential.

Potential.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .47 N-linked (GlcNAc. . .) (Pc
59800 MW; 1FF33F0AA52B97E4 CRC64;
                                                                                                                                                                                                                                                                                                               Cytoplasmic (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CIWA_HUMAN STANDARD; PRT; 538 AA. P57769; Q8TDK7; Q8TDK8; Q9HBS9; 16-0CT-2001 (Rel. 40, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 356 GNHNQELTPCRRTLSVNHLTNERDVLPP 383
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                                                                                                                                                                                                  Interpro; IPR003280; K+channel_2pore.
Interpro; IPR001622; K+channel_pore.
Interpro; IPR0018376; Trek_channel.
PRINTS; PR01333; 2POREKGTANEL.
PRINTS; PR01499; TREKCHANNEL.
                                                                                                                                                                                      EMBL; AF196965; AAF75132.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 63.7°
Matches 247; Conservative
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1180
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254
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538 AA;
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CIWA_HUMAN
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RN SEQUENCE FROM N.A. (ISOPORNUS B AND C).

RA GUNENCE FROM N.A. (ISOPORNUS B AND C).

RA GUNENCE FROM N.A. (ISOPORNUS B AND C).

RA GUNENCE FROM N.A. (ISOPORNUS B AND C).

RA GARGEDIN Detect C., Steinlein O.K., Daut J.;

REPORTION DETECT. (Steinlein O.K., Daut J.;

RY variants of the two-pore-domain potassium channel TREK-2.";

J. Physiol. (Lond.) 539:657-668(2002).

C. - FONCTION: Outward rectifying potassium channel. Produces rapidly activating and non-inactivating outward rectifier K(+) currents.

C. Activated by arachidonic acid and other naturally occurring unsaturated free fatty acids.

C. Activated by arachidonic acid and other naturally occurring unsaturated free fatty acids.

C. - SUBCELLULAR LOCATION: Integral membrane protein (Potential).

C. - ALTERNATIVE PRODUCTS:

C. - ALTERNATIVE PRODUCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is nor removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
        rectifying potassium
                                                                                                                                                                                                                                                                 Lesage F., Terrenoire C., Romey G., Lazdunski M.;
"Human TREK2, a 2P domain mechano-sensitive K+ channel with multiple
regulations by polyunsaturated fatty acids, lysophospholipids and Gs,
gi, and Gg protein-coupled receptors.";

J. Biol. Chem. 275:28398-28405(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM; 605873; ...
MIM; 605873; ...
MIM; 605873; ...
GO; GO:0005267; P:pocassium channel activity; TAS.
GO; GO:0006810; P:transport; TAS.
InterPro; IPR003280; K+channel 2pore.
InterPro; IPR003976; Trechennel pore.
InterPro; IPR003976; Trechennel.
PRINTS; PR01499; TREKCHANNEL.
PRINTS; PR01499; TREKCHANNEL.
PRINTS; PR01499; TREKCHANNEL.
POCASSIUM; Potassium; Potassium; Channel; Transport; Ionic channel; Voltage-gated channel.
                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Expressed in brain. SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.8) family.
                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM A).
MEDLINE=20435789; PubMed=10880510; DOI=10.1074/jbc.M002822200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pore-forming 1 (Potential)
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Potassium channel subfamily K member 10 (Outward rechannel protein TREK-2) (TREK-2 K+ channel subunit) Name-KCNK10; Synonyms-TREK2; Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Potential
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EMBL; AF385399; AAL95705.1; -.
EMBL; AF385400; AAL95706.1; -.
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154
182
203
234
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us-09-503-089a-2.rup

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Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Kroyninski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.,
                                                                                                                                                                                                                                                                                                              Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC075022; AAH75022.1; -.
EMBL; BC075021; AAH75021.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    543 AA; 60110 MW; 17DB1AFAPAB07C46 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 1243; DB 2;
; Pred. No. 7.9e-76;
54; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0016020; C:membrane; IEA.
GO; GO:000520f; F:ion channel activity; IEA.
GO; GO:000520f; F:ion channel activity; IEA.
GO; GO:00068013; P:potassium channel activity; II
GO; GO:0006813; P:potassium ion transport; IEA.
InterPro; IPR001280; K+channel_2pore.
InterPro; IPR01122; K+channel_pore.
InterPro; IPR011255; NiR SiRalpha_1/3.
InterPro; IPR003976; Trek_channel.
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25-0CT-2004 (TrEMBLrel. 28, Ls
25-0CT-2004 (TrEMBLrel. 28, Ls
LOCG46288 protein (Fragment).
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62.7%;
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Matches 247; Conservative
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Director MGC Project;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 FLUVVLYLIIGATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQIVAAI 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAGIIPLGNTSNQISHWDLGSSFFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLF 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KHIEGWSALDAIYFVVITLTTIGFGDYVAGG-SDIEYLDFYKPVVWFWILVGLAYFAAVL 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMIGDWLRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSIKRK 349
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    Pore-forming 2 (Potential).

Cycoplasmic (Potential).

N-linked (GlCNAc. . .) (Potential).
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TISSUE.

TISSUB-POOLED Tissue.

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                                                                                                                                                                                                                                                                                                                                                                          2 AAPDLLDPKSA-----AQNSKPRLSFSTKPTVLASRVESDT---TINVMKWKTVSTI
                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                          /FTIG=VSP_006697.
MFFLYTDFFLSL -> MKFPIETPRKQVNWDPK (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                    28;
                                                                                                                                                                                                                                                                                                  Length 538;
                                                                                                                                                                                                                                                                                                                                    65; Indels
                                                                                                                                                                                                isoform C).
/FTId=VSP_006698.
E -> G (in Ref. 2).
8EA615B08D147FBC CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Potassium channel, subfamily K, member 10, isoform 3. Name=KCNKIO;
                                                                                                                                                                                                                                                                                            59.2%; Score 1243; DB 1;
62.7%; Pred. No. 7.9e-76;
iive 54; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSAELAGNHNQELTPCRRTLSVNHLTNERDVLPP 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      543 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                          59764 MW;
                                                                                                                                                                                                                                                                                                                Best Local Similarity 62.78
Matches 247; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
        294
3319
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147
148
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                                                                                                                                                                                                                                                        538 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
        263
2299
320
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148
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                                                              CARBOHYD
CARBOHYD
CARBOHYD
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      DOMAIN
TRANSMEM
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                                                                                                                                                                              VARSPLIC
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                                                                                                                        VARSPLIC
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81 FVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDAD
                                                                                                                                                                                                                                                                                                                                                                                                                              FLVVVLYLIIGATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQIVAAI
                                                                                                                                                                                                                                          NAGIIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLF
                                                                                                                                                                                                                                                                 KHIEGWSALDAIYFVVITLTTIGFGDYVAGG-SDIEYLDFYKPVVWFWILVGLAYFAAVL
                                                                                                                  22 AAAPVCQPKSATNGQPPAPAPTPPRLSISSRATVVA-RMEGTSQGGLQTVMKWKTVVAI
                                                                                                                                                                                                                                                                                                                          GFLLAGVGDQLGTIFGKGIAKVEDTFIKMNVSQTKIRIISTIIFILFGCVLFVALPAIIF
                                                                                AAPDLLDPKSA-----AQNSKPRLSFSTKPTVLASRVESDT---TINVMKWKTVSTI
                                      Gaps
                                      28;
Length 543;
                                        65, Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQLGTIFGKGIAKVEDTF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
Name=LOC446288;
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                       MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                       "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.0%; Score 1217.5; DB 2; Length 546; 63.9%; Pred. No. 4.2e-74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klein S., Gerhard D.S.;
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC080069; AAH800069.1;
InterPro; IPR001280; K+channel 2pore.
InterPro; IPR00152; K+channel 2pore.
InterPro; IPR00152; K+channel 2pore.
PRINTS; PR01433; 2PORRKCHĀNEL.
PRINTS; PR01499; TREKCHĀNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60977 MW; AF6C7FB34AD34A06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90;
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                                                                                                                                                                                                                                            Dev. Dyn. 225:384-391(2002).
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Matches 235; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                    NCBI_TaxID=8355;
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                                                                                                                                                                                                                              initiative.
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SEQUENCE
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SEQUENCE FROM N.A. (ISOFORM 1).

MEDIANE=20231699; Pubmed=10767409; DOI=10.1016/S0014-5793(00)01388-0;
Lesage F., Maingret F., Lazdunski M.;

"Cloning and expersesion of human TRAAK, a polyunsaturated fatty acids-
315
                                                                     351
                                                                                                                                        EWTANVTABFKETRRILSVEIYDKFORATSIKRKLSAELAGNHNOELTPCRRTLSVNHLT 375
                                                                                                                                                                                PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;
PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;
Hillman R.T., Green R.E., Brenner S.E.;
"An unappreciated role for RNA surveillance.";
Genome Biol. 5:RESEARCH008.1-RESEARCH008 16 (2004)
-!-FUNCTION: Voltage insemilitive, instantaneous, outwardly rectifying potassium channel. Outward rectification is reversed at high external K(+) concentrations (By similarity).
-!-SUBUNIT: Homodiamer (Potential).
-!-SUBURID: Homodiamer (Potential).
-!-ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2004 (Rel. 44, Last annotation update)
05-UUL-2004 (Rel. 44, Last annotation update)
Potassium channel subfamily K member 4 (TWIK-related arachidonic acid-stimulated potassium channel protein) (TRAAK) (Two pore K+ channel
YVAGG-SDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVISKKTKEEVGEFRAHAA
                                        SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
MEDLINE=22179385; PUBMed=12191490; DOI=10.1016/S0169-328X(02)00157-2;
Ozatta A., Vega-Saenz de Mierza E.;
"Cloning of two transcripts, HKT4.1a and HKT4.1b, from the human two-pore K+ channel gene KCNK4. Chromosomal localization, tissue distribution and functional expression.";
Brain Res. Mol. Brain Res. 102:18-27(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=11042359; DOI=10.1016/S0169-328X(00)00183-2; Chapman C.G., Meadows H.J., Godden R.J., Campbell D.A., Duckworth M., Kelsell R.E., Murdock P.R., Randall A.D., Rennie G.I., Gloger I.S.; "Cloning, localisation and functional expression of a novel human, cerebellum specific, two pore domain potassium channel."; Brain Res. Mol. Brain Res. 82:74-83(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Assignment of KCNK4 encoding the human potassium channel TRAAK to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chromosome 11.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Event_Alternative splicing, Named isoforms=2; Name=1; Synonyms=KT4.la;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       activated and mechano-sensitive K(+) channel.";
FEBS Lett. 471:137-140(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       393 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=KCNK4; Synonyms=TRAAK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Frontal cortex;
                                                                                                                                                                                                                                                                                       376 NERDVLPP 383
                                                                                                                                                                                                                                                                                                                                                          397 HSLDMLSP 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CIW4 HUMAN
Q9NYG8; Q96T94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gray A.T.;
                                                                                                                                               316
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CIW4 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                 ACTIVATION
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                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||::|:|:|:|:|:|:|:|::||
61 LIKEVADALGGGADPETNSTSNSSHSAWDLGSAFFFSGTIITTIGYGNVALRTDAGRLFC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                            IsoId=Q9NYG8-2; Sequence=VSP 006689;
Note=May be produced at very low levels due to a premature stop codon in the mRNA, leading to nonsense-mediated mRNA decay;
SIMILARITY: Belongs to the two pore domain potassium channel
(TC 1.A.1.8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102 LIQQIVAAINAGIIPLGNTSNQISH--WDLGSSFFFAGTVITTIGFGNISPRTEGGKIFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              220 VLFVALPALIFKHIEGWSALDAIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLFVLTPTFVFCYMEDWSKLEAIYFVIVTLTTVGFGDYVAGADPRQDSPAYQPLVWFWIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160 IIYALLGIPLFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytoplasmic (Potential).
N-linked (GlonAc. . .) (Potential).
In-linked (GlonC. . .) (Potential).
M -> MTTAPQBPPARPLQAGSGAGPAPGRAM (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alternative splicing, Glycoprotein; Ion transport, Ionic channel,
Potassium, Potassium channel, Transmembrane, Transport,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38.2%; Score 803; DB 1; Length 393; 51.1%; Pred. No. 3e-46; ive 61; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VGLAYFAAVLSMIGDWLRVISKKTKEEVGEFRAHAAEWTANVTA 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytoplasmic (Potential).
Potential.
Pore-forming 2 (Potential).
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7F18E53A0A9AD57D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                          GO; GO:0005267; F:potassium channel activity; TGO; GO:0006813; P:potassium ion transport; TAS.
InterPro; IPR0013280; K+channel_pore.
InterPro; IPR001622; K+channel_pore.
InterPro; IPR0016074; TRAAK.Channel.
PRINTS; PR01333; 2POREKCHANNEL.
PRINTS; PR01691; TRAAKCHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              006689
IsoId=Q9NYG8-1; Sequence=Displayed;
me=2; Synonyms=KT4.1b;
                                                                                                                                                                                                                            or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Potential.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [soform 2]
                                                                                                                                                                                                                                                           EMBL, AF248242; AAG31731.1; -.
EMBL, AF247042; AAF64062.1; ALT_INIT.
EMBL, AF25500; AAK49380.1; -.
EMBL, AF259501; AAK49390.1; -?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42704 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 51.1<sup>§</sup>
Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                             Genew; HGNC:6279; KCNK4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Voltage-gated channel.
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CARBOHYD
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
                                                                                                                                                                                                                                                                                                                               "A neuronal two P domain K+ channel stimulated by arachidonic acid and polyunsaturated fatty acids.";
EMBO J. 17:3297-3308(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nat. Neurosci. 2:422-426(1999).
-!- FUNCTION: Voltage insensitive, instantaneous, outwardly rectifying potassium channel. Outward rectification is reversed at high external K(+) concentrations.
-! SUBMINI: Homodimer (Potential).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MISCELLANEOUS: Activated by arachidonic acid and other unsaturated fatty acids. Not affected by volatile general anaesthetics such as chloroform, diethyl ether, halothane and isoflurane.
                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-UTL-2004 (Rel. 44, Last annotation update)
Potassium channel subfamily K member 4 (TWIK-related arachidonic acidstimulated potassium channel protein) (TRAAK).
Name=Kcnk4; Synonyms=TRAAK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=2; Synonyms=TRAAKT, Truncated; Isode691; Isode6981; Isode698454-2; Sequence=VSP 006690, VSP 006691; TISSUE SPECIFICITY: Expressed in brain, spinal cord and eye. Not detected in heart, skeletal muscle, liver, lungs, kidney and
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lazdunski M.;
                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                 MEDLINE=98292450; PubMed=9628867; DOI=10.1093/emboj/17.12.3297;
Fink M., Lesage F., Duprat F., Heurteaux C., Reyes R., Fosset M.,
Lazdunski M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ion transport; Ionic channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-99254548; PubMed=10321245; DOI=10.1038/8084; Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M "Inhalational anesthetics activate two-pore-domain background K+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Potassium; Potassium channel; Transmembrane; Transport;
Voltage-gated channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Potential.
Pore-forming 1 (Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing; Named isoforms=2;
398 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=088454-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR0013280; K+channel 2pore.
InterPro; IPR001622; K+channel pore.
InterPro; IPR008074; TRAAK channel.
PRINTS; PR01333; 2POREKCHANDE.
PRINTS; PR01691; TRAAKCHANNEL.
Alternative splicing; Glycoprotein; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF056492; AAC40181.1; -.
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TC 1.A.1.8) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGI:1298234; Kcnk4
                                                                                                                                                                                                                                               SEQUENCE FROM N.A. TISSUE=Brain;
                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89
119
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DOMAIN
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Cytoplasmic (Potential). Potential. Pore-forming 2 (Potential). Potential. Cytoplasmic (Potential). N-linked (GlcNAc) (Potential). KILVE -> KAMAI (in isoform 2). /FTTd=VSP 006690. Missing (In isoform 2). /FTTd=VSP 006691. My; 478A834B7RAEC92 CRC64;	37.0%; Score 776.5; DB 1; Length 398; imilarity 49.8%; Pred. No. 1.9e-44; Conservative 57; Mismatches 83; Indels 3; Gaps 1; Mxwxrvsrrpi,xvx; TGATVEKAI.ROPHEISORTITIVIOKOPFISORSCVNSTELDE 101		LIQQIVAAINAGIIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIF 158 : : :	CIIYALLGIPLEGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFG 218 	CVLEVALPAIIFKHIBGWSALDAIYFVVITLTTIGFGDYVAGGSDIEXLDFYKPVVWFWI 278 -	LVGLAYFAAVLSMIGDWLRVISKKTKEEVGEFRAHAAEWTANVTA 323
171 1922 2222 2222 3988 811 84 67 398	37.0%; 49.8%; ative	ALVLLY	VAGIIP- GGANPE	PLFGFLL LFGMLL	IIFKHIE : :: :VFSYME	7LSMIGDW : : 7LTTIGNW
140 172 198 235 256 81 81 84 63 63	Similarity 49. 2; Conservative	MRSTTLLALI	LIQQIVAAINAGIIP :: : FIKLLVEALGGGANP	CIIYALLGII : CIFYALVGIE	CVLFVALPA] : CLLFVLTPTE	LVGLAYFAA\ : LFGLAYFAS\
DOMAIN TRANSMEM DOMAIN TRANSMEM DOMAIN CARBOHYD VARSPLIC VARSPLIC SEQUENCE	Query Match Best Local Sin Matches 142;	7 T	102	159	219	279
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Search completed: July 13, 2005, 08:44:29 Job time : 96.9622 secs

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July 13, 2005, 08:02:40; Search time 21.6316 Seconds (without alignments) 1828.118 Million cell updates/sec Run on:

US-09-503-089A-2 2100 Title: Perfect score:

1 MAAPDLLDPKSAAQNSKPRL.....LNGLTPHCAGEEIAVIENIK 411 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

) Description	inward rectifier p	TASK-5 protein - h	probable potassium	outward rectifier	potassium channel	hypothetical prote	hypothetical prote	probable potassium	potassium channel	hypothetical prote	hypothetical prote		_		_	_	_	_	_	_	_			probable potassium	hypothetical prote		hypothetical prote		hypothetical prote
SUMMARIES	ID	865566	JC7703	T43509	T32347	T13807	T23182	T19860	T43361	T43394	T25392	T45032	H88124	T15584	T24265	T21118	T27681	T26229	T30037	T28933	T23907	T21834	T26616	T21598	T43529	T16629	T22557	T26953	H89074	T24201
	DB	2	~	~	7	~	~	~	~	~	7	7	~	7	~	~	~	~	7	7	~	ď	~	~	~	N	~	~	N	7
	Length	336	330	329	336	1001	383	334	364	461	393	392	1910	325	522	452	427	444	1539	513	524	528	643	443	484	519	550	1136	307	485
d	ម្ង	18.1	16.5	16.4	15.8	•	13.7	13.5	13.5	•	13.3	13.0	13.0	12.8	12.7	12.5	11.9	11.8	11.7	11.6	11.4	11.3	11.2	11.0	10.9	10.9	10.8	10.7	10.4	10.4
	Score	379.5	347.5	345	331.5	319	288	284.5	284.5	282.5	279	273	273	269	266	262	249.5	247	245.5	244.5	240	236.5	236	230	228.5	228.5	227	224	218	218
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Cispecies: Homo maplems (man)
Cispecies: Homo sapiems (man)
Cispecies: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
Ciscossion: JG7703
Biochem. Biophys. Res. Commun. 284, 923-930, 2001
A;Title: TASK-5, a new member of the tandem-pore K+ channel family.
A;Reference number: JG7703; MUID:21303050; PMID:11409881

TASK-5 protein - human

RESULT

f22b7.7 protein - potassium channel hypothetical prote potassium channel potassium channel potassium channel outward-rectifler hypothetical prote hypothetical prote potassium channel hypothetical prote potassium channel	hypothetical prote hypothetical prote probable potassium
244635 143364 1713626 1743363 1246285 1246285 121683 1721551 1721550 1727550	T23700 T19429 T43531
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333 5544 576 691 586 500 500 500 500 500 500	539 681 569
011110111 00111110111 444444600000000000	9.00 9.00 9.00
217.5 217.5 217.5 217.5 217.5 217.5 215.5 215.5 205.5 205.5	202.5 196 195.5
6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	44 44 5

ALIGNMENTS

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inward rectifier potassium channel TWIK-1 - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004 C;Accession: S6556 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004 R;Lesage, F; Guillemare, E.; Fink, M.; Duprat, P.; Lazdunski, M.; Romey, G.; Barhanin, EMBO J. 15, 1004-1011, 1996 #sequence number: S65566; MUID:96183184; PMID:8605869 A;Accession: S6556 #sequence: MUID:96183184; PMID:8605869 A;Accession: S6556 #sext MAD:8605869 A;Accession: S6556 #sequence: MUID:96180184; PMID:91086490; PIDN:AAB01688.1; PID:910 A;Cross-references: UNIPROT:000180; EMBL:U33632; NID:91086490; PIDN:AAB01688.1; PID:910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 FLVV---VLYLIIGATVFKALEQPHEISQRITIVIQKQTFISQHSCVNSTELDELIQQIVA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109 AINAGIIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIP 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          169 LFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTII--FILFGCVLFVALP 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  227 AIIFKHIE-GWSALDAIYFVVITLTTIGFGDYVAG-GSDIEYLDFYKPVVWFWILVGLAY 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         200 AAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQKFRELYKIGITCYLLLGLIA 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 FLVLGYLLIYLVFGAVVFSSVELPYEDLLRQELRKLKRRFLEEHECLSEQQLEQFLGRVLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 18.1%; Score 379.5; DB 2; Length 336; Best Local Similarity 32.5%; Pred. No. 3.5e-23; Matches 90; Conservative 62; Mismatches 108; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       260 MLVVLETFCE-LHELKKFRKMFYVKKDKDEDQVHIIE 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                285 FAAVLSMIGDWLRVISK----KTKEEVGEFRAHAAE
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A;Cross-references: UNIPROT:017185; EMBL:AF025454; PIDN:AAC71151.1; GSPDB:GN00020; CESP:
A;Experimental source: strain Bristol N2; clone F34D6
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          potassium channel protein - fruit fly (Drosophila melanogaster)

C;Species: Drosophila melanogaster

C;Species: Drosophila melanogaster

C;Date: 13-Aug-1999 #Sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C;Accession: T13807

R;Goldstein, S.A.; Price, L.A.; Rosenthal, D.N.; Pausch, M.H.

R;Goldstein, S.A.; Price, L.S.A.; 93, 13256-13261, 1996

A;Title: ORKI, a potassium-selective leak channel with two pore domains cloned from Dros
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1001 (GGL>
A;Cross-references: UNIPROT:Q94526; EMBL:U55321; NID:g3808067; PID:g3808068; PIDN:AAC69:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIEGGKIFCIIYALLGIPLFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIIS 210
GWGGLLIFGGAFMFSSYENWTYFDAVYYCFVTLTTIGFGDYVALQKRGSLQTQPEYV-FF 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93 CVNSTELDELIQQIVAAI--NAGIIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGNISP 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :| | | : | : | | | | DLIIPCTGWGGLLIFGGAFWFSSYENWTYFDAVYYCFVTLTTIGFGDYVALQKRGSLQTQ 223
                                                                                                                                                                                                                                                                                                                                outward rectifier potassium channel homolog twk-23 - Caenorhabditis elegans C;Species: Caeloris Species: Caeloris Species: Caeloris Species: Caeloris Caelo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----RTTIVIQKQTFISQHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIIFILFGC-VLFVALPALIFKHIEGWSALDAIYFVVITLTTIGFGDYVA---GGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Introns: 44/3; 102/1; 136/1; 180/1; 207/1; 265/2; 296/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.8%; Score 331.5; DB 2; 32.9%; Pred. No. 2.8e-19; ative 56; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42 MKWKTVSTIFLVV--VLYLIIGATVFKALEQPHEISQ--
                                                                                                                                              223 SLV---FILFGLTVISAAMNLL--VLRFLTMNTEDE
                                                                                                            271 KPVVWFWILVGLAYFAAVLSMIGDWLRVISKKTKEE
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A;Cross-references: PlyBase:FBgn0017561
A;Map position: 1
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Best Local Similarity 32.9*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Gene: twk-23; CESP:F34D6.3
A,Map position: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 211
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      A;Molecule type: DNA
A;Residues: 1-330 «KIM»
A;Cross-references: GB:AL118522
C;Comment: This protein, a new member of the tandem-pore K+ channel family with four transcention, but does not produce a functional plasma membrane K+ current by itsel C;Comment: task-5
A;Gene: task-5
A;Map position: 20q12
C;Keywords: transmembrane segment #status predicted <TMS1>
F;7.30/Domain: transmembrane segment #status predicted <TMS2>
F;107-128/Domain: transmembrane segment #status predicted <TMS2>
F;129-155/Region: hydrophobic cytoplasmic linker #status predicted
F;5.56-180/Domain: transmembrane segment #status predicted <TMS3>
F;220-240/Domain: transmembrane segment #status predicted <TMS3>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               167 IPLFGFLLAGVGDQLGTIFGKGIAKVEDTF-IKWNVSQTKIRIISTIIFILFGCVLFVAL 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         226 PAIIFKHIEGWSALDAIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWF---WILVGL 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 DELIQQIVAAI--NAGIIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKI 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 FCMLYALAGIPLGLIMFQSIGERMNTFAAKLL----RFIRRAAGKQPIVTSSDLIFCT 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               218 GC-VLFVALPAIIFKHIEGWSALDAIYFVVITLTTIGFGDYVA---GGS---DIEYLDFY 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable potassium channel chain n2P38 - Caenorhabditis elegans C,Species: 21-Jan-2000 #text_change 09-Jul-2004 (C,Accesion: T43509 R;Wang, Z.W.; Salkoff, L. submitted to the EMBL Data Library, August 1998 A,Description: Potassium channels in C. elegans. A,Reference number: Z22450 A,Reference number: Z22450 A,Status: preliminary; translated from GB/EMBL/DDBJ A,Molecule type: mRNA A,Molecule type: mRNA A,Molecule type: mRNA A,Residues: 1-329 cWAN> A,Cross-references: UNIPROT:017185; EMBL:AF083652; PIDN:AAG32863.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50 IFLVVVLYLIIGATVFKALEQPHEISQRTTIVIQKQTFISQ---HSCVNSTELDELIQQI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 16.5%; Score 347.5; DB 2; Best Local Similarity 34.9%; Pred. No. 1.4e-20; Matches 91; Conservative 42; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.4%; Score 345; DB 2; Lk
33.7%; Pred. No. 2.2e-20;
ive 56; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 283 AYFAAVLSMI -----GDW 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | | :::
TVIGAFLNLVVLRFLVASADW 253
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Best Local Similarity 33.7%;
Matches 93; Conservative
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50 IFLVVVLYLIIGATVFKALEQPHEISQRTTIV---IQKQTFISQHSCVNSTELDELIQQI 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166 GIPLFGFLLAGVGDQLGTIFGKGIAKVEDTFIK-----WNVSQTKIRIIS-TIIFILFG 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            219 CVLFVALPAIIFKHIEGWSALDAIYFVVITLTTIGFGDYV--AGGSDIEYLDFYKPVVWF 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 306 ACFFYCLSNVSSIVVRQLLNWM---IKKMDVKV-EDRSFLC------FKKKRRRYMGL 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    277 WILVGLAYFAAVLSMIGDWLRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRLSVEI 336
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.-----VLGFMASNADEVTA-----AQREPPSAIV 273
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A;Generozzo:
A;Map position: X
A;Introns: 34/1; 60/2; 98/1; 145/3; 160/3; 181/1; 204/1; 252/2; 279/2; 306/3
                                                                                                                                                                                                         Appothetical protein C40C9.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T1980
R;Hembry, C.
Submitted to the EMBL Data Library, March 1996
A;Reference number: Z19188
A;Recession: T19860
A;Recession: T19860
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Recule: type: DNA
A;Residues: 1-334 < WIL.
A;Residues: BMBL:Z70266; PIDN:CAA94204.1; GSPDB:GN00028; CESP:C40C9.
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T43361
R;Wang, Z.W.; Salkoff, L.
submitted to the EMBL Data Library, August 1998
A;Reference number: Z22450
A;Reference number: Z22450
A;Accession: T43361
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Wolecule type: mRNA
A;Residues: 1-364 <WANA
A;Cross-references: UNIPROT:O76790; EMBL:AF083646; PIDN:AAC32857.1
            -----AAVLSMIGDWLRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRLSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     234 FILIGLAVFSACVNLL----
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27.4%;
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Best Local Similarity
Matches 86; Conserv
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Best Local Similarity
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C.Species: T3-0Ct-1999 #text_change 09-Jul-2004
C.Accession: T22182
R.Dobson, R.
R.Dobson, R.
A.Reference number: 219703
A.Reference number: T23182
A.Reference number: T23182
A.Residues: T23182
A.Residues: 1-383 *WIL>
A.Res
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                                                                                                                          50 IFLVVVLYLIIGATVFKALEQPHE----ISQRTTIVIQKQTFISQHSCVNSTELDELIQQ 105
                                                                                                                                                                                                                                              106 IVAAINAGIIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALL 165
                                                                                                                                                                                                                                                                                GIPLFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVS-----QTKIRIISTIIFILF-G 218
                                                                                                                                                                                                                                                                                                                                                                                                    219 CVLFVALPAIIFKHIEGWSALDAIYFVVITLTTIGFGDYVA------GGSDIBYLD 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FYKPVVWFWILVGLAYFAAVLSMIGDWLRVISKK----TKEEVGEFRAHAAEWTANVTAE 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SATVISTIGFGISTPRTHLGRFITIVYGVVGCTCCVLFFNLFL----ERLVTGMSYLRS 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      246 TASAGIYSUVENWNYIDSLYFCFISFATIGFGDYVSNQQDVTRMSPDLYRFVNFCLLTLG 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGTVITTIGFGNISPRTEGGKIFCIIYALLG----IPLFGFLLAGVGDQLGTIFGKGIAK 191
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                                                                                                                                                                                    9 LLIFYISYLMFGAAIYYHIEHGEEKISRAEQRKAQIAINEYLLEELGDKNTTTQDEILQR 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IALFLLPSWVFTYFENWPYSISLYYSYVTTTTGFGDYVPTFGANQPKEFGGWFVVYQI
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                                                                      Gaps
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                                                                36;
         Length 1001;
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      ; Score 319; DB 2; Length 10; Pred. No. 1.1e-17; 61; Mismatches 127; Indels
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         15.2%;
ilarity 28.4%;
Conservative 6
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Query Match
Best Local Similarity
Matches 89; Conserv
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Best Local Similarity
Matches 85; Conserv
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                                                                      50 IFLVVVLYLIIGATVFKALEQPHEISQRTTIV---IQKQTFISQHSCVNSTELDELIQQI 106
                                                                                                                                                                                                        107 VAAINAGIIPLGNTSNQISH-WDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALL 165
                                                                                                                                                                                                                                                                                                                                             GIPLFGFLLAGVGDQLGTIFGKGIAKVEDTFIK-----WNVSQTKIRIIS-TIIFILFG 218
                                                                                                                                                                                                                                                                                                                                                                                    120 GVPMGLIMFQSIGERVNTFIAYSLHKFRDSLHQQGFTCLQEVTPTHLLMVSLTIGEWV-- 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               219 CVLFVALPAIIFKHIEGWSALDAIYFVVITLTTIGFGDYV--AGGSDIEYLDFYKPVVWF 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----IVSGTYMFHTIEKWSIFDAYYFCMITFSTIGFGDLVPLQQVNALQDQPLYVFATIM 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    277 WILVGLAYFAAVLSMIGDWLRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEI 336
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A.Reference number: Z22479
A.Reference number: Z22479
A.Residues: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Residues: 1-461 <KUN>
A.Kesidues: J-461 <KUN>
A.Cross-references: UNIPROT:Q18120; EMBL:AF083650; PIDN:AAC32861.1
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       23;
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   63; Mismatches 112; Indels
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234 FILIGLAVFSACVNLL---
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       Conservative
       86;
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submitted to the EMBL Data Library, March 1997
A;Reference number: 220027
A;Accession: T25392
A;Accession: T25392
A;Actus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-393 <WILL>
A;Cross-references: UNIPROT: Q9XU07; EMBL: Z92813; PIDN: CAB07286.1; GSPDB: GN00021; CESP:T2
A;Experimental source: clone T28A8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ģ
337 VDPEEDPENNKKSFDAV--ISRMNWSKRGLYYLLPDSQKKELAKQSEKKMGRKSIKIQ-- 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : | : : | : : | : | : | : | : | 64 EMRESGIGQHVVEDLAVKYVDNVTRILFEAFDTHCIGAKHLRPGGEDEDYNWTYMTALFF 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGD-----QLGTIFGKG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----IRIISTIIFILFGCVL-FVALPAIIFKHI 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGWSALDAIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIG 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63
                                                                                                                                                                                                                                                           hypothetical protein T28A8.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Beate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T25392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 WKTYARIILAHVSLIVLSVVYVGFGAFLFYQLBQPNEVEVRARNIERFNIHKRQMIEHLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --QHSCVNSTELDELIQQIVAAINAGIIPLGNT-----SNQISHWDLGSSPPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44 WKTVSTIFL-----VVVLYLIIGATVFKALEQPHEISQRTTIV----IQKOTFIS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 13.3%; Score 279; DB 2; Length 393
Best Local Similarity 27.0%; Pred. No. 6.1e-15;
Matches 81; Conservative 54; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: CESP:T28A8.1
A;Map position: 3
A;Introns: 73/1; 112/3; 179/2; 209/3; 287/2; 310/3; 364/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189 IAKVEDTFIKWNVSQTK----
                                                               375 TNERDVLPPLLKTE 388
                                                                                                - | : | |:: |
-TDNDLLETLIREE
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hypothetical protein Y39B6B.f [imported] - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000 C;Accession: T45032

R;Wilson, R.; Ainscough, R.; Anderson, K.; Baynes, C.; Berks, M.; Bonfield, J.; Burton, raser, A.; Fulton, L.; Gardner, A.; Green, P.; Hawkins, T.; Hillier, L.; Jier, M.; Johns B.; O'Callaghan, M.; Parsons, J.; Percy, C.; Rifken, L.; Roopra, A.; Saunders, D. Nature 368, 32-38, 1994

A, Authors: Shownkeen, R.; Sims, M.; Smaldon, N.; Smith, A.; Smith, M.; Sonnhammer, B.; tock, L.; Wilkinson-Sproat, J.; Wohldman, P. A; Title: 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans. A; Reference number: \$43531; MUID:94150718; PMID:7906398

A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA

A;Residues: 1-392 <WIL>
A;Cross-references: EMBL:AL132896; NID:g6434440; PIDN:CAB60911.1; PID:g6434446
A;Experimental source: clone Y39B6B

A;Map position: 3 A;Introns: 47/2; 82/2; 106/3; 151/1; 220/1; 260/3; 370/3 A;Note: Y39B6B.£	Db 339 TTMATIGYGNIVPVTPLGRLACVLFALFGAPIALITIGDLGKPLSECTIWLYKHWRKGSA 398 Qy 191 KVEDTFIKW
Query Match 13.0%; Score 273; DB 2; Length 392; Best Local Similarity 25.5%; Pred. No. 1.9e-14; Matches 83; Conservative 66; Mismatches 100; Indels 76; Gaps 13;	Db 399 RLDSAWKRFRGLEDSISDDLESASKNQDSSILDMDWDBIDKSEVPVLMVFTIIL 452 QY 221 LFVALPAIFFKHIEGWSALDAIYFVVILTIGFGDYVAGGSDIBYLDFYKPVVWFWILV 280
Qy 7 LDPKSAAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVVLY 57	
Qy 58 LIIGATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQI-V 107	Db 507 GLSVTTMCIDLAGIQYIQKIHYFGRKFQGTDLLQYLKKKRMLERRLAMGQGEEILRKYVH 566 Ov 314 AAEWTANVTAEFKETRRRLSVEIYDK 339
QY 168 PLFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTI 212 : : : : : : :	RESULT 13 T15584 hypothetical protein C24A3.6 - Caenorhabditis elegans C;Species: Caenorhabditis elegans
Qy 213 IFILFGCVLFV-ALPALIFKHIE-GWSALDAIYFVVITLTTIGFGDYVAGGS-DIEYLDF 269 : : :	C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999 C;Accession: T15584 R;Favello, T. R;Favello, T. submitted to the EMBL Data Library, November 1995
Qy 270 YKDVVWFWILVGLAYFAAVLSMIGD 294 Db 325 YKIGATVYLMGGLCCMMLFLATLYD 349	A; Description: The sequence of C. elegans cosmid C24A3. A; Reference number: 218373 A; Accession: T15584 A; Status: preliminary; translated from GB/EMBL/DDBJ
RESULT 12 H88124 protein T12C9.3 (imported) - Caenorhabditis elegans	A;Molecule type: DNA A;Residues: 1-325 <fav> A;Cresidues: 1-325 <fav> A;Cresidues: BMBL:U40424; NID:g1065542; PID:g1065543; PIDN:AAA81455.1; CESP:C24A C;Genetics: A;Gene: CESP:C24A3.6</fav></fav>
C;Species: Caenorhabditis elegans C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001 C;Accession: H88124 R;anonymous, The C. elegans Sequencing Consortium.	A;Introns: 21/1; 63/3; 131/1; 193/3; 206/3 Query Match Best Local Similarity 25.1%; Pred: No. 3.1e-14;
A;Note: genome sequence of the nematode C. elegans: a platform for investigating biolog A;Itle: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A75000; MUID:99069613; PMID:9851916 A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www sanger.ac.uk/Projects/C_ele A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and	QY 46 TVSTIFLVVVLYLIGATVERALEQPHEISQRTTIVIQKQTFISQHSCVN 95
A,Accession: H88124 A,Status: prefininary A,Molecule type: DNA A,Residues: 1-1910 <sto></sto>	Qy 96 STELDELIQQIVAAIN
0 1	OY 126 HWDLGSSFFPAGTVITTIGFGNISPRTEGGKIFCLIYALLGIPLFGFLLAGVGDQLGTIF 185
2 13.0%; Score 273; DB 2; Length 1910; ilarity 23.3%; Pred. No. 1.2e-13;	Qy 186 GKGIAKVEDTFIKMNVSQTKIRIIS
Matches 104; Conservative 74; Mismatches 122; Indels 146; Gaps 18; Qy 18 PRLSPSTKPTVLAS-RVESDTTINVMKWTVSTIFLVVVLYLLIGATVFKA 67 Dh 152 Docember Poort Peabphorement Alternative Mill	Qy 211TIIFILFGCVLFVALPAIIFKHIEGWSALDAIYFVVITLTTIGFGDYVAGGSDIEXL 267 223 LSFPISGLLLITVIWVIFCAVLFTFLEBWDFGTSLYFTLISFTTIGFGDILPSDYDFM 280
68 LEQPHEISQRITIVIQKQTFISQHSCVNSTELD	Qy 268 DFYKPVVWFWILVGLAYFAAVLSMIGDWLRVISKKTKE 305
Qy 105 QIVAAINAGIIPLGYSNQISHWDLGSSFFFAG 137	RESULT 14 T24265 T24265 Campulation T01B4.1 - Caenorhabditis elegans
Qy 138 TVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQLGTIFGKGIA 190	C:Species: Caenorhabdilis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C;Accession: T24265

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Matches
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T21118
hypotherical protein F19D8.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21118
R;Swinburne, J.; Ainscough, R.
submitted to the EMBL Data Library, August 1996
A;Reference number: Z19377
A;Accession: T21118
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;References: UNIPROT:Q93531; EMBL:Z78541; PIDN:CAB01740.1; GSPDB:GN00028; CESP:P1
A;Experimental source: clone F19D8
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;App position: X
A;Introns: 31/1; 82/2; 101/3; 157/1; 197/1; 230/3; 267/2; 325/3; 356/1; 404/3
R;Wilkinson, J.
submitted to the EMBL Data Library, March 1996
A;Reference number: Z19866
A;Recession: T24265
A;Accession: T24265
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Residues: 1-522 <WILL>
A;Residues: 1-522 <WILL>
A;Cross-references: UNIPROT:Q22042; EMBL:Z70036; PIDN:CAA93875.1; GSPDB:GN00028; CESP:TC
A;Experimental source: clone T01B4
C;Generics: A;Gene: CESP:T01B4.1
A;Map position: X
A;Introns: 95/3; 142/1; 224/3; 290/1; 458/1
                                                                                                                                                                                                                                                                                                                                                                                                      ::: | |: | |: | |: | |: | |- |- |- KRCLELITKTFIQRSDERGEGWRWDFWNSVFFSATIFTTIGYGNLACKINLGRI 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---OLGTIFGKG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IAKV------EDTF--IKWNVSQTKIRIISTIIFILFGCVLFVALPAIIFKHIEGWS 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261 FLTAFYPFFVSLSTIGFGDIVP------DHPRTACALFVLYFIGLALFAMVYAILQER 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----- 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        323 AEFKETRRRLS-----VEIYDKFQRATSIKRKLSAEL-----AGNHNQELTPCRRTLS 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALDALYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWIL--VGLAYFAAVLSMIGD- 294
                                                                                                                                                                                                                                                                                                                                                                            98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              99 LDELIQQIVAAINAGIIPLGNTS-NQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKI
                                                                                                                                                                                                                                                                                           Query Match 12.7%; Score 266; DB 2; Length 522;
Best Local Similarity 23.1%; Pred. No. 9.7e-14;
Matches 99; Conservative 64; Mismatches 132; Indels 134; Gaps
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216 MLEVFEVPEDDKEDTTFQLRWG---
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Length 452;

12.5%; Score 262; DB 2; 28.5%; Pred. No. 1.7e-13;

Query Match Best Local Similarity

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| Matches | 81; | Conservative | 50; | Mismatches | 121; | Indels | 32; | Gaps | 7; | Conservative | 50; | Mismatches | 121; | Indels | 32; | Gaps | 7; | Conservative | Co
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Search completed: July 13, 2005, 08:45:40 Job time : 24.6316 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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2100
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 18, Appl	Sequence 2, Appli	Sequence 83, Appl	Sequence 2, Appli	Sequence 31, Appl	Sequence 83, Appl	Sequence 83, Appl	Sequence 20, Appl	Sequence 45, Appl	Sequence 45, Appl	Sequence 57, Appl
SUMMARIES	US-09-892-360-18	US-09-828-746-2	US-10-121-746-83	US-10-745-210-2	. US-10-349-528-31	US-10-976-644-83	US-10-976-647-83	US-10-349-528-20	US-08-816-011-45	US-10-870-492-45	US-10-870-492-57
8	: :	σ	14	16	.91	17	17	16	8	17	17
% Query Match Length DB	411	411	411	411	411	411	411	422	426	426	426
% Query Match	100.0	99.8	99.8	99.8	8.66	99.8	99.8	99.2	98.2	98.2	98.0
Score	2100	2095	2095	2095	2095	2095	2095	2089	2062	2062	2058
Result No.	-	7	٣	4	2	9	7	æ	6	10	11

GATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQIVAAINAGIIPLGNT 120

61

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	Sequence Seq	360 A STRETCH-AND ARACHIDONIC ACID-SENSITIVE ACTIVATED BY INHALATIONAL ANESTHETICS AND 9/892,360 ,559	100.0%; Score 2100; DB 11; Length 411; ; Conservative 0; Mismatches 0; Indels 0; Gaps 0; MAAADDLLDPKSAAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIPLVVVLYLII 60
US-10-870-492-58 US-10-870-492-59 US-09-828-746-6 US-09-939-484-8 US-09-939-483-8 US-09-939-483-8 US-09-930-483-8 US-09-729-920-5 US-10-129-920-4 US-09-729-920-4 US-09-729-920-4 US-09-729-920-4 US-09-729-920-4 US-09-729-920-4 US-09-729-920-4 US-09-729-920-2 US-10-923-035-46 US-10-923-035-46 US-10-923-035-46 US-10-923-035-46 US-10-923-035-46 US-10-923-035-46 US-10-923-035-46 US-10-923-920-2 US-10-923-920-2 US-10-923-920-2 US-10-923-920-2 US-10-923-920-2 US-10-923-920-2 US-10-923-920-2 US-10-923-920-2 US-10-923-920-2 US-10-923-920-2 US-10-923-920-2 US-10-923-920-2 US-10-932-93-93-93-93-93-93-93-93-93-93-93-93-93-	US-09-828-03 US-09-828-03 US-10-345-05 US-10-352-06 US-10-352-07 US-10-351-33 US-10-852-77 US-10-852-77 US-10-852-77 US-10-852-77 US-10-852-77	19892360 1A1 1EK2, A STRETCH- INEL ACTIVATED E 1B 1US/09/892,360 1G-27 1714,559	; Score 2100; ; Pred. No. 3 0; Mismatche RLSFSTKPTVLASR RLSFSTKPTVLASR
22244444444444444444444444444444444444	2	Application US/09892 Application US/09892 MATION: AZDUNSKI, MICHEL ICHANNEL ENTION: ENTION: RILUZOLE ICATION NUMBER: CE: 1256-R-00 ICATION NUMBER: OD ATE: 2001-06-27 ATION NUMBER: 60/214 ID NOS: 25 tentin Ver: 2.1	100.0%; imilarity 100.0%; ; Conservative 0; MAAPDLLDPKSAAQNSKPRLS
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GATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQIVAAINAGIIPLGNT 120
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Publication No. US20030036648A1

GENERAL INFORMATION:

APPLICANT: Miller, Andrew P.

APPLICANT: Miller, Andrew P.

APPLICANT: Hu, Ping

APPLICANT: Hu, Ping

APPLICANT: Riller, Mark Edward

APPLICANT: Ruther, Marc

APPLICANT: Wang, Jian-Wang

TITLE OF INVENTION: No. US20030036648A1e1 Human Potassium Channels

TITLE OF INVENTION: No. US20030036648A1e1 Human Potassium Channels

FURENET FILING DATE: 1002-04-11

PRIOR APPLICATION NUMBER: US/10/121,746

PRIOR PELLING DATE: BARLIER FILING DATE: 1999-06-18

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/116,448

PRIOR PELLING DATE: EARLIER FILING DATE: 1999-01-19

PRIOR PELLING DATE: EARLIER FILING DATE: 1999-01-19

PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-01-19

PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-02-22

NUMBER OF SEQ ID NOS: 87

FENCINE APPLICATION OF 83

SOFTWARE: FARESE FOR Windows Version 4.0

SEQ ID NOS: 87
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Best Local Similarity 99.8
Matches 410; Conservative
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US-10-121-746-83
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JOHNERAL INFORMATION:
JOHNERAL INFORMATION:
JOHNERAL CONTROL GERALD CHAPMAN
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30031-D1
CURRENT APPLICATION NUMBER: US/09/828,746
CURRENT FILING DATE: 1999-01-25
PRIOR FILING DATE: 1999-01-25
PRIOR FILING DATE: 1998-01-27
PRIOR FILING DATE: 1998-01-27
PRIOR FILING DATE: 1998-01-27
PRIOR FILING DATE: 1998-01-27
SPRIOR FILING DATE: 1998-01-27
SOFTWARE: FESTESC FOR WINDOWS: 6
SOFTWARE: FASTESC FOR WINDOWS VERSION 3.0
SEQ ID NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09828746
Patent No. US20020028485A1
GENERAL INFORMATION:
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ORGANISM: HOMO SAPIENS
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APPLICANT: Miller, Andrew P.
APPLICANT: Hiller, Ping
APPLICANT: Hu, Ping
APPLICANT: Rutter, Marc
APPLICANT: Wang, Jian Wang
ITILE OF INVENTION: Novel Human Potassium Channels
FILE REPERENCE: SEQ-15P
CURRENT APPLICATION NUMBER: US/09/976,644
CURRENT FILING DATE: 2004-10-29
FRIOR PELING DATE: 1999-06-18
PRIOR FILING DATE: 1999-06-18
PRIOR FILING DATE: 1999-07
PRIOR APPLICATION NUMBER: 60/116,448
PRIOR PILING DATE: 1999-01-19
PRIOR APPLICATION NUMBER: PCT/US99/03826
PRIOR FILING DATE: 1999-01-19
PRIOR PILING DATE: 1999-01-19
SROID NOS: 87
SOFTWARE: FASTSEQ for Windows Version 4.0
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                                Score 2095; DB 16;
Pred. No. 1.1e-187;
1; Mismatches 0;
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                                  99.8%;
                                Query Match
Best Local Similarity 99.8
Matches 410; Conservative
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Best Local Similarity 99.8
Matches 410; Conservative
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US-10-976-644-83
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Publication No. US20040253668A1
GENERAL INCOMMATION:
GENERAL INCOMMATION:
GENERAL INCOMMATION:
APPLICANT: RAWANNATHAN, Chandra
APPLICANT: GOPAL, Shuba
APPLICANT: FINITE, Gabe
APPLICANT: FEDER, John
TITLE OF INVENTION: USE THEREOF
FILE REPREMENTS: DOJJO
TITLE OF INVENTION NUMBER: US/10/349,528
CURRENT APPLICATION NUMBER: US/10/349,528
CURRENT PILING DATE: 2003-01-22
NUMBER OF SEQ ID NOS: 35
SOFTWARR: Patentin version 3.2
SEQ ID NO 31
LENGTH: 411
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                                                             APPLICANT: TONOII, Giulio
APPLICANT: TONOII, Chiara
TITLE OF INVENTION ION CHANNELS AS TARGETS FOR SLEEP-RELATED DRUGS
FILE REFERENCE: 054030-0004
CURRENT APPLICATION NUMBER: US/10/745,210
FRIOR APPLICATION NUMBER: US 60/436,201
RRIOR PILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 2
SOFTHAME: PATENTIN NOS: 2
SOFTHAME: PATENTIN VERSION 3.2
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Sequence 2, Application US/10745210
Publication No. US20040143855A1
GENERAL INFORMATION:
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Matches 410; Conservative
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US-10-745-210-2
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LENGIH: 411
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us-09-503-089a-2.rapb

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DEPLICANT: RAMANATHAN, Chandra
APPLICANT: RAMANATHAN, Chandra
APPLICANT: GOPAL, Shuba
APPLICANT: GOPAL, Shuba
APPLICANT: MINIER, Gabe
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR (GPCR) VARIANTS AND METHODS OF
TITLE OF INVENTION: USE THEREOF
TITLE OF INVENTION: USE THEREOF
CURRENT APPLICATION NUMBER: US/10/349,528
CURRENT APPLICATION NUMBER: US/10/349,528
SURRENT FILING DATE: 2003-01-22
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin version 3.2
SEQ ID NO 20
              ALYFVVITLITIGEGDYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS 300
                                                                                KKTKEEVGEFRAHAAEWTANVTAEFKETRRLSVEIYDKFQRATSIKRKLSAELAGNHNQ 360
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                                                                                                                                                                    Length 422;
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Pred. No. 4.1e-187;
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3; Mismatches
                                                                                                                                                                                                                                                                     Sequence 20, Application US/10349528; Publication No. US20040253668A1; GENERAL INFORMATION:
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US-08-816-011-45
Sequence 45, Application US/08816011
; Publication No. US20030165806A1
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Matches 408; Conservative
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US-10-349-528-20
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US-10-349-528-20
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Sequence 83, Application US/10976647

Publication No. US20050112663A1

GENERAL INFORMATION:

APPLICANT: Miller, Andrew P.

APPLICANT: Miller, Andrew P.

APPLICANT: Hu, Ping

APPLICANT: Rutter, Mark Edward

APPLICANT: Rutter, Mark Edward

APPLICANT: Rutter, Mark Edward

APPLICANT: Rutter, Mark Edward

APPLICANT: Wang, Jian-Wang

TITLE OF INVENTION: Novel Human Potassium Channels

FILE REFERENCE: SEQ-15P

CURRENT APPLICATION NUMBER: US/10/976,647

CURRENT APPLICATION NUMBER: COM-10-29

PRIOR FILING DATE: 1998-08-07

PRIOR APPLICATION NUMBER: 60/076,687

PRIOR APPLICATION NUMBER: 60/076,687

PRIOR APPLICATION NUMBER: 60/116,448

PRIOR PILING DATE: 1999-01-10

PRIOR PILING DATE: 1999-02-22

NUMBER OF SEQ ID NOS: 87

SOFTWARE: FastSEQ for Windows Version 4.0

SETUNGENT 414
                                                                    SNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ
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Pred. No. 1.1e-187;
1; Mismatches 0;
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Best Local Similarity 99.8
Matches 410; Conservative
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US-10-976-647-83
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98.2%;
98.5%;
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Matches 405, Conservative
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ORGANISM: Homo sapiens
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             APPLICANT: Price, Laura A. APPLICANT: Pausch, Mark H. TITLE CANT: Pausch, Mark H. TITLE OF INVENTION: Potassium Channels, Nucleotide Sequences TITLE OF INVENTION: Encoding Them, and Methods of Using Same NUMBER OF SEQUENCES: 56 CORRESPONDENCE ADDRESS: AMERICAN HOME Products Corporation STREET: One Campus Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 426;
                                                                                                                  ADDRESSEE: American Home Products Corporation STREET: One Campus Drive CITY: Paratappany STATE: New Jersey COUNTRY: USA ZIP: 07054 EPOPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/816,011 FILING DATE: IL-MAR 1997 CLASSIFICATION: 536 ATTORNEY/AGENT INPORMATION: NAME: 32,269 REGISTRATION NUMBER: 32,269 REGISTRATION NUMBER: 32,269 REGISTRATION INFORMATION: TELEBRAK: 201-683-2134 TELEBRAK: 201-683-4117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 2062; DB 8;
Pred. No. 1.4e-184;
3; Mismatches 3;
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US-10-870-492-45
; Sequence 45, Application US/10870492
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Best Local Similarity 98.5%;
Matches 405; Conservative
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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JAPPLICANT: PAUSCH, MARK H.

TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLECTIDE SEQUENCES ENCODING THEM,
TITLE OF INVENTION: ADM METHODS OF USING SAME
TILLE OF INVENTION: ADM METHODS OF USING SAME
TILLE REPERENCE: 01142.0114 SEQUENCE LISTING
CURRENT APPLICATION NUMBER: US/10/870,492
CURRENT APPLICATION NUMBER: US/99/503,849
PRIOR FILING DATE: 2000-02-15
PRIOR FILING DATE: 1997-03-11
PRIOR FILING DATE: 1997-03-11
PRIOR FILING DATE: 1995-10-25
PRIOR FILING DATE: 1994-10-31
NUMBER OF SEQ ID NOS: 74
SOOFWARE: Patentin Ver. 2.1
SEQ ID NO 45
LENGTH: 426
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Publication No. US20050032165A1
GENERAL INFORMATION:
APPLICANT: PAUSCH, MARK H.
TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
TITLE OF INVENTION: AND METHODS OF USING SAME
FILE REPRENCE: 01142.0114 SEQUENCE LISTING
CURRENT FILING DATE: 2004-06-18
PRIOR FILING DATE: 2000-02-15
PRIOR FILING DATE: 2000-02-15
PRIOR FILING DATE: 1997-03-11
PRIOR PLILING DATE: 1997-03-11
PRIOR PLILING DATE: 1997-03-11
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Pred. No. 1.4e-184;
3; Mismatches 3;
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: PAUSCH, MARK H.

TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,

TITLE OF INVENTION: AND METHODS OF USING SAME

TITLE OF INVENTION: AND METHODS OF USING SAME

FILE REFERENCE: 01142.0114 SEQUENCE LISTING

CURRENT PILING DATE: 2004-06-18

FRICR APPLICATION NUMBER: US/09/503,849

FRICR APPLICATION NUMBER: 08/816,011

FRICR APPLICATION NUMBER: 08/816,011

FRICR APPLICATION NUMBER: PCT/US95/14364

FRICR APPLICATION NUMBER: 07/332,312

FRICR FILING DATE: 1995-10-25

FRICR FILING DATE: 1994-10-31

NUMBER OF SEQ ID NOS: 74
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Gaps
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Pred. No. 8e-184;
3; Mismatches 4; Indels 0
Indels
  4; Mismatches
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  Conservative
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CAGANISM: Homo sapiens
US-10-870-492-60
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US-10-870-492-60
    404;
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Publication No. US20050032165A1
GENERAL INFORMATION:
TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
TITLE OF INVENTION: AND METHODS OF USING SAME
TITLE OF INVENTION: AND METHODS OF USING
CURRENT PILING DATE: 2004-06-18
FILE REPERENCE: 01142.0114 SEQUENCE LISTING
CURRENT APPLICATION NUMBER: US/10/870,492
CURRENT APPLICATION NUMBER: US/09/503,849
PRIOR FILING DATE: 2000-02-15
PRIOR FILING DATE: 1997-03-11
PRIOR FILING DATE: 1997-03-11
PRIOR FILING DATE: 1995-10-25
PRIOR APPLICATION NUMBER: PCT/US95/14364
PRIOR APPLICATION NUMBER: 07/332,312
PRIOR FILING DATE: 1994-10-31
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PARCHIN VET. 2.1
SEQ ID NO 58
LENGTH + 426
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                                                                                                                                                                                                                                 Query Match 98.0%; Score 2058; DB 17; Length 426; Best Local Similarity 98.3%; Pred. No. 3.4e-184; Matches 404; Conservative 3; Mismatches 4; Indels 0
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Pred. No. 4.2e-184;
PRIOR FILING DATE: 1995-10-25
PRIOR APPLICATION WUMBER: 07/332,312
PRIOR FILING DATE: 1994-10-31
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PALENLIN Ver. 2.1
SEQ ID NO 57
LENGTH: 426
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98.3%;
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                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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US-10-870-492-58
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Search completed: July 13, 2005, 09:07:00 Job time : 92.2442 secs
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US-09-828-746-6
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                                                                                                                                                                                                                           Sequence 59, Application US/10870492

| Publication No. US20050032165A1
| GENERAL INFORMATION:
| APPLICANT: PAUSCH, MARK H.
| TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
| TITLE OF INVENTION: ADM METHODS OF USING SAME
| FILE REFERENCE: 01142.0114 SEQUENCE LISTING
| CURRENT APPLICATION NUMBER: US/10/492
| CURRENT FILING DATE: 2004-06-18
| PRIOR PLILING DATE: 2000-02-15
| PRIOR PLILING DATE: 1997-03-11
| PRIOR FILING DATE: 1997-03-11
| PRIOR FILING DATE: 1995-10-25
| PRIOR FILING DATE: 1994-10-31
| NUMBER OF SEQ ID NOS: 74
| CONTUMER OF SEQ ID NOS: 74
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                                                241 AIYFVVITLITIGEGDYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS 300
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Pred. No. 9.9e-184;
4; Mismatches 4;
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98.1%;
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Matches 403; Conservative
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US-10-870-492-59
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61 GAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS 120
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361 ELTPCRRTLSVNHLTNERDVLPPLLKTESIYLNGLTPHCAGEEIAVIENIK
                                        376 ELTPCRRTLSVMHLTSERDVLPPLLKTESIYLNGLAPHCAGEEIAVIENIK
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96.9%; Score 2035; DB 9;
Best Local Similarity 95.9%; Pred. No. 4.6e-182;
Matches 394; Conservative 12; Mismatches 5;
                                                                                                                                                                                                                              Sequence 6, Application US/09828746
Fatent No. US20020028485A1
GENERAL INFORMATION:
FAPPLICANT: Helen Jane Meadows
APPLICANT: Conrad Gerald Chapman
TITLE NET INVENTION: NOVEL COMPOUNDS
FILLE REFERENCE: GP-30031-D1
CURRENT APPLICATION NUMBER: US/09/828,746
CURRENT FILING DATE: 1999-01-25
FRIOR APPLICATION NUMBER: US 09/236,080
FRIOR FILING DATE: 1998-01-25
FRIOR FILING DATE: 1998-01-25
FRIOR FILING DATE: 1998-01-27
FRIOR FILING DATE: 1998-01-37
FRIOR FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
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Sequence 6, Appli
Sequence 4, Appli
Sequence 67, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 7, Appli
Sequence 3, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 16, Appli
Sequence 3, Sequence 16, Appli
Sequence 16, Appli
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US-09-949-016-7794
US-09-362-842-6
US-09-362-842-6
US-09-362-842-6
US-09-370-767-4542
US-09-370-767-4542
US-09-362-842-2
US-09-561-763-11
US-09-561-763-11
US-09-144-914-7
US-09-144-914-7
US-09-144-914-6
US-09-362-842-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tch 99.8%; Score 2095; DB 3; al Similarity 99.8%; Pred. No. 4.7e-205; 410; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Helen Meadows
APPLICANT: Helen Meadows
TITLE OF INVENTION: No. 642217el Compounds
FILE REFERENCE: GP30031
CURRENT APPLICATION NUMBER: US/09/236,080
CURRENT FILING DATE: 1999-01-25
NUMBER OF SEC ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LEMOTH: 411
TYPE: PRT
                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                         US-09-236-080-2; Sequence 2, Application US/09236080; Patent No. 6242217; GENERAL INFORMATION:
 ; ORGANISM: Homo sapiens
US-09-236-080-2
   284
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Best Local S:
Matches 410
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2, Appli
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Sequence 8, Appli
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1 MAAPDLLDPKSAAQNSKPRL.......INGLTPHCAGEEIAVIENIK 411
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(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/ReCOMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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US-09-144-914-2
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Matches 394; Conservative
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                                                  ; ORGANISM: Mus musculus
US-09-236-080-6
                                                                                                                                   Similarity
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ORGANISM: Murine
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US-09-144-914-8
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J. Sequence 83, Application US/09336643A

J. Sequence 83, Application US/09336643A

J. Ratent No. 6399761

J. GENERAL INFORMATION:

APPLICANT: Miller, Andrew P.

APPLICANT: Willer, Marc

APPLICANT: Rutter, Marc

APPLICANT: Wang, Jian-Wang

TITLE OF INVENTION: No. 6399761el Human Potassium Channels

TITLE OF INVENTION: No. 6399761el Human Potassium Channels

FILE REFERENCE: SEQ.15P

CURRENT APPLICATION NUMBER: US/09/336,643A

FILE REPLICATION NUMBER: 60/076,687

PRIOR PRILING DATE: 1999-08-07

PRIOR FILING DATE: 1999-01-19

PRIOR FILING DATE: 1999-01-19

PRIOR FILING DATE: 1999-02-22

NUMBER OF SEQ ID NOS: 87

SOFTWARE: FastSEQ for Windows Version 4.0

1.ENGTH: 411
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Patent No. 6242217
GENERAL INFORMATION:
APPLICANT: Helen Meadows
APPLICANT: Conrad Chapman
TITLE OF INVENTION: No. 6242217el Compounds
FILE REFERENCE: GP30031
CURRENT APPLICATION NUMBER: US/09/236,080
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Best Local Similarity 99.8
Matches 410; Conservative
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US-09-236-080-6
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Sequence 8, Application US/09144914

Sequence 8, Application US/09144914

Patent No. 6309855

GENERAL INFORMATION:

APPLICANT: Duprat, Fabrice

APPLICANT: Lesage, Florian

APPLICANT: Lasdunski, Michel

APPLICANT: Laddunski, Michel

TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING

TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS

FILE REFERENCE: 989.6705CIP

CURRENT FPLING DATE: 1998-09-01

EARLIER APPLICATION NUMBER: 08/749,816

EARLIER FILING DATE: 1996-01

EARLIER FILING DATE: 1996-04

EARLIER FILING DATE: 1996-04

EARLIER FILING DATE: 1996-06

EARLIER FILING DATE: 1996-06

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EARLIER FILING DATE: 1996-06

SEALIER FILING DATE: 1996-07

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SERVILER FILING DATE: 1996-07

SERVILER FILING DATE: 1996-06

SERVILER FILING DATE: 1996-06

SERVILER FILING DATE: 1996-07

SERVILER FILING DATE: 1996-06

SERVILER FILING DATE: 1996-07

SERVILER FILING DATE: 1996-
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                                                                                                                                                                                                                                                                                                                                                                                      96.9%; Score 2035; DB 3;
95.9%; Pred. No. 6.2e-199;
tive 12; Mismatches 5;
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
LENGTH: 411
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Sequence 7368, Application US/09949016;
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
ITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
ITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                            GFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAIIF 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 FLVVVLYLIIGATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQIVAAI 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KHIEGWSALDAIYFVVITLTTIGFGDYVAGG-SDIEYLDFYKPVVWFWILVGLAYFAAVL 289
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                        196 GFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPAVIF
                                                                        KHIEGWSALDAIYFVVITLTTIGFGDYVAGG-SDIEYLDFYKPVVWFWILVGLAYFAAVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 NAGIIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLF
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                                                                                                                                                                                                                   350 LSAELAGNHNOELTPCRRTLSVNHLTNERDVLPP 383
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 7368
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US-09-949-016-7368
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Sequence 7001, Application US/09949016

Sequence 7001, Application US/09949016

Sequence 7001, Application US/09949016

Sequence 7001, Application US/09949016

SERRAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: G0/241,755

PRIOR PAPLICATION NUMBER: G0/241,755

PRIOR PELING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: G0/231,498

PRIOR APPLICATION NUMBER: G0/231,498

PRIOR APPLICATION NUMBER: G0/231,498

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SGO ID NO 7001

LENGTH: 538
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                                                                                                                           GATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQIVAAINAGIIPLGNT 120
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                                                                                                                                                                                                                                                                                          181 LGTIFGKGIAKVEDTFIKMNVSQTKIRIISTIIFILFGCVLFVALPAVIPKHIEGWSALD
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                                                                                                                                                                                                                                                                                                                                                                                                                   KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSIKRKLSAELAGNHNQ
                                                    1 MAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVVLYLII
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                    Indels
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 Pred. No. 1.8e-177;
8; Mismatches 5;
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62.7%; Pred. No. 6.1e-118;
ive 54; Mismatches 65;
96.5%;
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Matches 247; Conservative
Best Local Similarity 96.5
Matches 355, Conservative
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361 ELTPCMRT 368
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ORGANISM: Human
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Query Match
Best Local Similarity 51.1%
Matches 145; Conservative
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US-09-949-016-6913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 LIQQIVAAINAGIIPLGNTSNQISH--WDLGSSFFFAGTVITTIGFGNISPRTEGGKIFC 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160 IIYALLGIPLEGELLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGC 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  220 VLFVALPALIFKHIEGWSALDAIYFVVITLTIGFGDYVAGGSDIEYLDFYKPVVWFWIL 279
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                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 38.2%; Score 803; DB 4; Length 39
Best Local Similarity 51.1%; Pred. No. 3e-73;
Matches 145; Conservative 61; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 4, Application US/09432470; Patent No. 6426197; GENERAL INFORMATION: APPLICANT: David Malcolm Duckworth APPLICANT: David Malcolm Duckworth; APPLICANT: Conrad Gerald Chapman; TITLE OF INVENTION: NOVEL COMPOUNDS FILE REPERENCE: GP-30190; CURRENT FILING DATE: 1999-11-03
EARLIER APPLICATION NUMBER: UK 9223668.9
EARLIER PILING DATE: 1999-10-07
EARLIER FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASESEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 393
                                                                                                              APPLICANT: David Malcolm Duckworth
APPLICANT: Conrad Gerald Chapman
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30190
CURRENT APPLICATION NUMBER: US/09/432,470
CURRENT FILING DATE: 1999-11-03
EARLIER PELION NUMBER: UK 9923668.9
EARLIER APPLICATION NUMBER: UK 9824048.4
EARLIER PILING DATE: 1999-10-07
EARLIER PILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FRAESEQ FOR WINGOWS Version 3.0
                                                               Sequence 2, Application US/09432470 Patent No. 6426197 GENERAL INFORMATION:
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US-09-432-470-4
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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOOL307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR PILING DATE: 2000-04-14
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                42 MKWKTVSTIFLVVVLYLIIGATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDE 101
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                                                                                                                                                                                                                  LIQQIVAAINAGIIPLGNTSNQISH--WDLGSSFFFAGTVITTIGFGNISPRTEGGKIFC 159
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                                                        Indels
38.2%; Score 803; DB 4; L
51.1%; Pred. No. 3e-73;
iive 61; Mismatches 76;
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Gaps

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127 LIWI-SALGKFFGGRAKRLGQFLTKRGVSLRKAQITCTVIFIVWGVLVHLVIPPFVFMVT 185
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                                                                       | SIN SYNOVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Curtis, Rory A.J. et al.
TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR TILE REFERENCE: MII-074CP2
CURRENT APPLICATION NUMBER: US/09/561,763
CURRENT FILING DATE: 2000-04-29
FRIOR FILING DATE: 01-11-1999
PRIOR FILING DATE: 01-11-1999
PRIOR FILING DATE: 01-03-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54 VVLYLIIGATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQIVAAINAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    174 LAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAIIFKHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 EGWNYIEGLYYSFITISTIGFGDFVAGVNPSANYHALYRYFVELMIYLGLAW----LSLF
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Patent No. 6670149
Patent No. 6670149
Patent No. 6670149
TITLE INFORMATION:
APPLICANT: Curtis, Roxy A.J.
TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR FILE REPERENCE: MNI-074CP
CURRENT APPLICATION NUMBER: US/09/431,367B
CURRENT FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: 09/259,951
                                                                                                                                    179 DQLGTIFGKGIAKVEDTFIKMNVSQTKIRIISTIIFILFGCVLFVAL 225
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0; Indels
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Mismatches
                                                                                                                                                                                                                                                                                            ; Sequence 2, Application US/09561763; Patent No. 6664373
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                                          119 NTSNQISHWDLGSSFFFAGTVI
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31.1%;
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Best Local Similarity 31.1;
Matches 106; Conservative
105; Conservative
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SOFTWARE: Patentin Ver. 3
SEQ ID NO 2
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US-09-431-367B-2
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                                                                       Sequence 7809, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: WENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF PILE REPERENCE: CL0013307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 MKWKTVSTIFLVVVLYLIIGATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDE 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 LIQQIVAAINAGIIPLGNTSNQISH--WDLGSSFFFAGTVITTIGFGNISPRTEGGKIFC 159
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Pred. No. 5.6e-48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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APPLICANT: Conrad Chapman
TITLE OF INVENTION: No. 6242217el Compounds
FILE REFERENCE: GP30031
CURRENT APPLICATION NUMBER: US/09/236,080
CURRENT FILING DATE: 1999-01-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38.2%; Score 803;
51.1%; Pred. No. 3
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SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 7809
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PELING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PELING DATE: 2000-09-08
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98.1%;
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Best Local Similarity 51.1*
Matches 145; Conservative
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Best Local Similarity
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US-09-431-367B-5
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Best Local S:
Matches 89
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                                                                                                                                                                                                      54 VVLYLIIGATVFKALEOPHEISORTTIVIOKOTFISOHSCVNSTELDELIQQIVAAINAG 113
                                                                                                                                                                                                                                                                    114 IIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFL 173
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                                                                                                                                                                                                                                                                                                                                                   293 GDWLRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSIKRKLSA 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: CURTIS, RORY A.J. et al.
TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR TITLE REPERENCE: MNI-074CP2
CURRENT APPLICATION NUMBER: US/09/561,763
CURRENT FILING DATE: 2000-04-29
PRIOR APPLICATION NUMBER: 09/431,367
PRIOR APPLICATION NUMBER: US 09/431,367
PRIOR PLING DATE: 01-11-1999
PRIOR PLING DATE: 01-03-1999
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                          Gaps
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                                                                                                                                           DB 4; Length 499;
                                                                                                                                        Query Match 20.3%; Score 427; DB 4; Length 49
Best Local Similarity 31.1%; Pred. No. 1e-34;
Matches 106; Conservative 60; Mismatches 121; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242 VNW------KVSMF-----VEVHKAIKKRRRR-----
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Patent No. 6664373
GENERAL INFORMATION:
PRIOR FILING DATE: 1999-03-01
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN VEY. 2.0
SEQ ID NO 2
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                                                                             TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 89; Conserv
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SOFTWARE: Pack
SEQ ID NO 5
                                                                                                             US-09-431-367B-2
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US-09-561-763-5
                                                               LENGTH: 499
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170 FGFLLAGVGDQLGTIFGKGI----AKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVAL 225
50 IFLVVVLYLIIGATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQIVAA 109
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9. Sequence 5. Application US/09431367B

9. Fatent No. 6670149

9. GENERAL INFORMATION:

1. APPLICANT: Curtis, Rory A.J.

1. APPLICANT: Curtis, Rory A.J.

1. TILLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR TILLE OF INVENTION NUMBER: US/09/431,367B

1. CURRENT APPLICATION NUMBER: US/09/431,367B

1. CURRENT PILING DATE: 1999-11-01

1. PRIOR FILING DATE: 1999-03-01

1. NUMBER OF SEQ ID NOS: 12

1. SOFTWARE: PATCHIN VET. 2.0

1. SEQ ID NO 5.
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; Pred. No. 2.5e-31;
51; Mismatches 94; Indels
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35.9%;
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ORGANISM: Homo sapiens
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